



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1109098562-18357-122032509583.BLASTQ2

Query=

(378 letters)

SEQ ID NO: 2

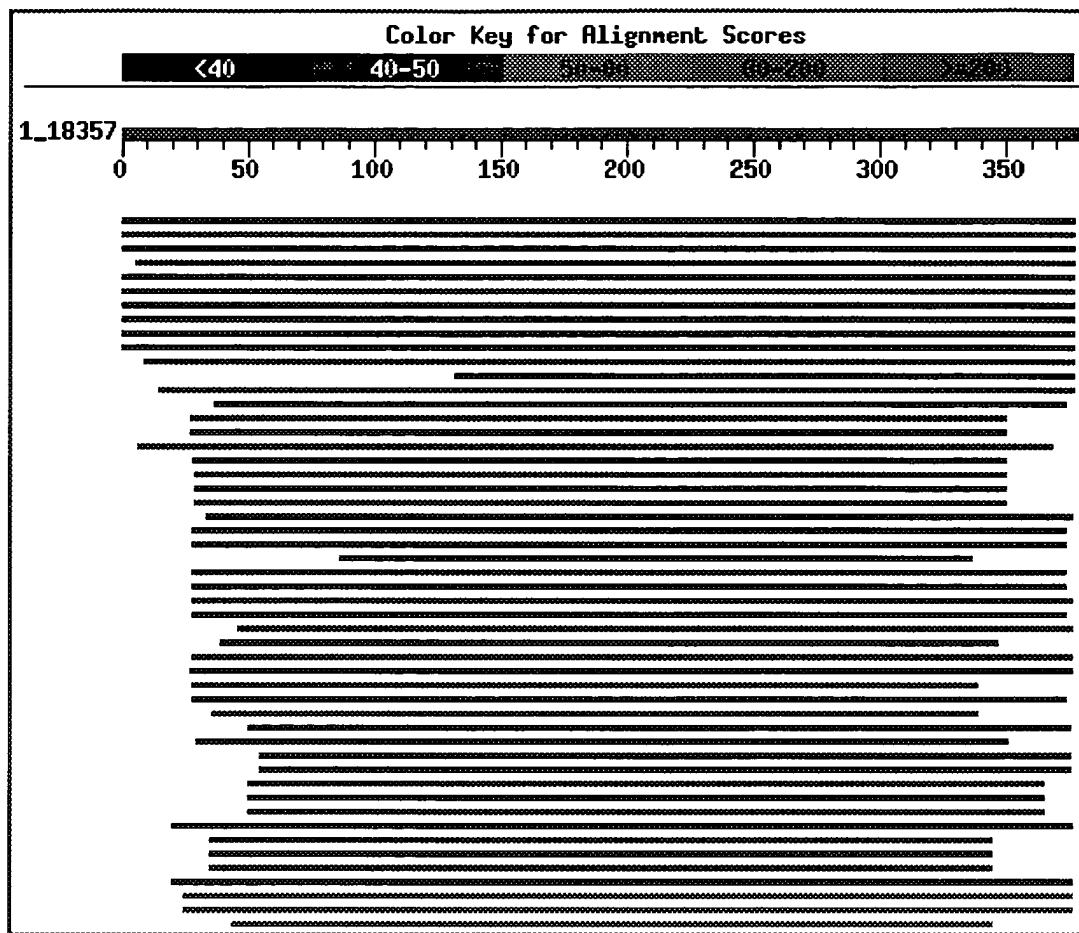
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,331,049 sequences; 790,373,496 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 501 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



²⁴ See, for example, the discussion of the 1993 Constitutional Commission in the *South African Journal of International Law* 1994, 111-120.

Score (bits)	E Value
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gi 422826 pir A45680	G protein-coupled peptide receptor EB...	688	0.0	G
gi 4502641 ref NP_001829.1	chemokine (C-C motif) receptor ...	682	0.0	G
gi 31127005 gb AAN47099.2	CC chemokine receptor 7 [Macaca ...	675	0.0	
gi 55645367 ref XP_511477.1	PREDICTED: chemokine (C-C moti...	669	0.0	G
gi 56553516 gb AAV97930.1	chemokine receptor 7 [Bos taurus]	635	0.0	
gi 48374059 ref NP_001001532.1	chemokine (C-C motif) recep...	634	e-180	G
gi 57091575 ref XP_548131.1	PREDICTED: similar to chemokin...	625	e-178	G
gi 26332358 dbj BAC29909.1	unnamed protein product [Mus mu...	603	e-171	G
gi 6671772 ref NP_031745.1	chemokine (C-C motif) receptor ...	601	e-171	G
gi 58477681 gb AAH89762.1	Chemokine (C-C motif) receptor 7...	601	e-170	G
gi 50760889 ref XP_425875.1	PREDICTED: similar to CC chemo...	421	e-116	G
gi 33415854 gb AAQ18436.1	chemokine receptor 7 [Bos taurus]	409	e-113	G
gi 49118818 gb AAH73273.1	MGC80638 protein [Xenopus laevis]	375	e-102	G
gi 47223975 emb CAG06152.1	unnamed protein product [Tetrao...	286	9e-76	
gi 14043042 ref NP_112477.1	chemokine (C-C motif) receptor...	251	2e-65	G
gi 14043044 ref NP_006632.2	chemokine (C-C motif) receptor...	251	2e-65	G
gi 57101682 ref XP_541909.1	PREDICTED: similar to chemokin...	250	4e-65	G
gi 6753462 ref NP_034043.1	chemokine (C-C motif) receptor ...	247	3e-64	G

gi 27229230 ref NP_758832.1	chemokine (C-C motif) receptor...	247	4e-64	
gi 48675913 ref NP_001001624.1	chemokine C-C motif recepto...	245	1e-63	
gi 41688290 dbj BAD08644.1	chemokine (C-C motif) receptor ...	245	1e-63	
gi 34853814 ref XP_217862.2	similar to G protein-coupled r...	231	2e-59	
gi 1668738 emb CAB02144.1	G PROTEIN-COUPLED RECEPTOR CKR-L...	229	1e-58	
gi 37188165 ref NP_113597.2	chemokine (C-C motif) receptor...	229	1e-58	
gi 47221187 emb CAG05508.1	unnamed protein product [Tetrao...	229	1e-58	
gi 55627742 ref XP_527565.1	PREDICTED: chemokine (C-C moti...	228	2e-58	
gi 1870669 gb AAC51125.1	G protein-coupled receptor [Homo ...	228	2e-58	
gi 24137229 gb AAN47098.1	CC chemokine receptor 6 [Macaca ...	228	3e-58	
gi 6753318 ref NP_033965.1	chemokine (C-C motif) receptor ...	228	3e-58	
gi 2655885 emb CAA05917.1	chemokine receptor [Oncorhynchus...	227	5e-58	
gi 50741692 ref XP_419608.1	PREDICTED: similar to C-C chem...	226	8e-58	
gi 5478218 dbj BAA82443.1	CC Chemokine LARC specific recep...	223	5e-57	
gi 57032273 ref XP_541197.1	PREDICTED: hypothetical protei...	223	7e-57	
gi 34740125 dbj BAC87714.1	C-C chemokine receptor 9 [Paral...	222	1e-56	
gi 1515435 gb AAB06949.1	IL8-related receptor [Homo sapiens]	221	2e-56	
gi 47212478 emb CAF90274.1	unnamed protein product [Tetrao...	217	4e-55	
gi 48675917 ref NP_001001623.1	chemokine C-X-C motif recep...	214	2e-54	
gi 52354647 gb AAH82897.1	LOC494782 protein [Xenopus laevis]	213	7e-54	
gi 11342662 gb AAG34367.1	chemokine receptor CXCR6 [Mus mu...	213	9e-54	
gi 13507658 ref NP_109637.1	chemokine (C-X-C motif) recept...	211	4e-53	
gi 59857715 gb AAX08692.1	G protein-coupled receptor TYMST...	207	3e-52	
gi 59857629 gb AAX08649.1	G protein-coupled receptor TYMST...	205	2e-51	
gi 59858157 gb AAX08913.1	G protein-coupled receptor TYMST...	204	3e-51	
gi 30795217 ref NP_848540.1	chemokine (C-C motif) receptor...	204	4e-51	
gi 15028430 gb AAK81712.1	chemokine receptor CCR11 [Mus mu...	203	6e-51	
gi 26326635 dbj BAC27061.1	unnamed protein product [Mus mu...	202	1e-50	
gi 21746187 ref NP_663746.1	chemokine (C-C motif) receptor...	202	1e-50	
gi 55621142 ref NP_526311.1	PREDICTED: chemokine (C-C moti...	202	2e-50	
gi 59857673 gb AAX08671.1	chemokine (C-C motif) receptor-1...	198	2e-49	
gi 27806269 ref NP_776690.1	chemokine (C-C motif) receptor...	197	3e-49	
gi 42557662 emb CAF28781.1	C-C chemokine receptor 9 like [...]	197	5e-49	
gi 50733072 ref XP_426014.1	PREDICTED: similar to C-C chem...	197	5e-49	
gi 50978648 ref NP_001003020.1	CC chemokine receptor 4 [Ca...	196	9e-49	
gi 2258402 gb AAB64225.1	Bonzo [Cercopithecus aethiops] >g...	194	3e-48	
gi 4877755 gb AAD31419.1	chemokine receptor bonzo [Macaca ...	194	3e-48	
gi 32481999 gb AAP84352.1	chemokine receptor 4 [Homo sapie...	194	4e-48	
gi 50733078 ref XP_426017.1	PREDICTED: similar to CC chemo...	194	4e-48	
gi 6467137 dbj BAA86966.1	b-chemokine receptor CCR4 [Homo ...	194	4e-48	
gi 6467141 dbj BAA86968.1	b-chemokine receptor CCR4 [Homo ...	194	4e-48	
gi 26449155 ref NP_598216.2	chemokine (C-C) receptor 4 [Ra...	193	6e-48	
gi 13430093 gb AAK25742.1	orphan seven transmembrane recep...	193	6e-48	
gi 2258400 gb AAB64224.1	Bonzo [Macaca nemestrina] >gi 312...	193	8e-48	
gi 7716472 gb AAF68392.1	STRL33 [Cercocebus torquatus atys]	192	1e-47	
gi 57113977 ref NP_001009051.1	chemokine (C-X-C motif) rec...	192	2e-47	
gi 915274 gb AAA92582.1	chemokine receptor [Mus musculus]	191	3e-47	
gi 32482007 gb AAP84356.1	chemokine receptor 6 [Homo sapie...	190	5e-47	
gi 10716828 gb AAG21918.1	mutant G protein-coupled recepto...	190	5e-47	

gi 50760178 ref XP_417922.1	PREDICTED: similar to putative...	190	6e-47	G
gi 6857773 ref NP_034046.1	chemokine (C-C motif) receptor ...	189	1e-46	G
gi 2209288 gb AAB61457.1	G protein-coupled receptor STRL33...	189	1e-46	G
gi 18034375 gb AAL57488.1	CC-chemokine receptor 4 [Cavia p...	187	4e-46	
gi 340784 emb CAA48723.1	MDCR15 protein [Homo sapiens] >gi...	187	4e-46	G
gi 56553518 gb AAV97931.1	chemokine receptor 3 [Bos taurus...	187	5e-46	G
gi 5514619 gb AAD44012.1	CC chemokine receptor type 5 [Cer...	187	5e-46	
gi 5713011 gb AAD47707.1	C-C chemokine receptor 5 [Macaca ...	186	7e-46	
gi 6753458 ref NP_034040.1	chemokine (C-X-C motif) recepto...	186	7e-46	G
gi 27753515 gb BAC55184.1	CXC chemokine receptor 3 [Capra...	186	7e-46	
gi 5514617 gb AAD44010.1	CC chemokine receptor type 5 [Cer...	186	7e-46	
gi 5713013 gb AAD47709.1	C-C chemokine receptor 5 [Macaca ...	186	9e-46	
gi 5514623 gb AAD44016.1	CC chemokine receptor type 5 [Cer...	186	9e-46	
gi 5514622 gb AAD44015.1	CC chemokine receptor type 5 [Cer...	186	9e-46	
gi 3282810 gb AAC40163.1	chemokine receptor CXCR3 [Mus mus...	186	9e-46	G
gi 14589869 ref NP_116743.1	Burkitt lymphoma receptor 1 is...	186	1e-45	G
gi 4502415 ref NP_001707.1	Burkitt lymphoma receptor 1 iso...	186	1e-45	G
gi 5579304 gb AAD45497.1	CC chemokine receptor type 5 [Cer...	186	1e-45	
gi 5713106 gb AAD47802.1	C-C chemokine receptor 5 [Cercopi...	185	2e-45	
gi 5713039 gb AAD47735.1	C-C chemokine receptor 5 [Macaca ...	185	2e-45	
gi 33578093 gb AAQ22367.1	CC chemokine receptor 5 [Macaca ...	185	2e-45	
gi 4406111 gb AAD19862.1	C-C chemokine receptor type 5 [Ma...	185	2e-45	
gi 5713068 gb AAD47764.1	C-C chemokine receptor 5 [Varecia...	185	2e-45	
gi 12407353 gb AAG53465.1	CC chemokine receptor type 5 [Ce...	185	2e-45	
gi 57111007 ref XP_536065.1	PREDICTED: similar to interleu...	184	3e-45	G
gi 5713098 gb AAD47794.1	C-C chemokine receptor 5 [Cercopi...	184	3e-45	
gi 5713044 gb AAD47740.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713043 gb AAD47739.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713035 gb AAD47731.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713031 gb AAD47727.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713029 gb AAD47725.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713028 gb AAD47724.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713017 gb AAD47713.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5579302 gb AAD45495.1	CC chemokine receptor type 5 [Cer...	184	3e-45	
gi 5514618 gb AAD44011.1	CC chemokine receptor type 5 [Cer...	184	3e-45	
gi 4102994 gb AAD01639.1	G-protein coupled chemokine recep...	184	3e-45	
gi 13873087 gb AAK43369.1	C-C chemokine receptor 5 [Miopit...	184	3e-45	
gi 2088633 gb AAC34132.1	chemokine receptor CCR5 [Macaca m...	184	3e-45	
gi 5713016 gb AAD47712.1	C-C chemokine receptor 5 [Macaca ...	184	4e-45	
gi 4894982 gb AAD32685.1	CC chemokine receptor 5 [Papio cy...	184	4e-45	
gi 13873073 gb AAK43362.1	C-C chemokine receptor 5 [Erythr...	184	4e-45	
gi 42475950 ref NP_031577.2	Burkitt lymphoma receptor 1 [M...	184	5e-45	G
gi 5713110 gb AAD47806.1	C-C chemokine receptor 5 [Erythro...	184	5e-45	
gi 5713105 gb AAD47801.1	C-C chemokine receptor 5 [Cercopi...	184	5e-45	
gi 5713069 gb AAD47765.1	C-C chemokine receptor 5 [Lemur c...	184	5e-45	
gi 5713045 gb AAD47741.1	C-C chemokine receptor 5 [Macaca ...	184	5e-45	
gi 5713033 gb AAD47729.1	C-C chemokine receptor 5 [Macaca ...	184	5e-45	
gi 5579303 gb AAD45496.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 5514621 gb AAD44014.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 5514615 gb AAD44008.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 4426827 gb AAD20555.1	CC chemokine receptor 5 [Cercopit...	184	5e-45	
gi 2347108 gb AAC51795.1	CC chemokine receptor-5 [Cercopit...	184	5e-45	
gi 1002741 gb AAC50505.1	GPR9	183	6e-45	G
gi 4504099 ref NP_001495.1	chemokine (C-X-C motif) recepto...	183	6e-45	G
gi 5713112 gb AAD47808.1	C-C chemokine receptor 5 [Erythro...	183	6e-45	
gi 5713108 gb AAD47804.1	C-C chemokine receptor 5 [Erythro...	183	6e-45	

gi 5713100 gb AAD47796.1	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713090 gb AAD47786.1	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713081 gb AAD47777.1	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713065 gb AAD47761.1	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 31455576 gb AAP55851.1	C-X-C chemokine receptor transcript...	183	6e-45	G
gi 2305194 gb AAB65738.1	CCR5 receptor [Pan troglodytes]	183	6e-45	G
gi 5514620 gb AAD44013.1	CC chemokine receptor type 5 [Cer...	183	6e-45	
gi 3135302 gb AAC39833.1	chemokine receptor CCR5 [Cercoceb...	183	6e-45	
gi 5713099 gb AAD47795.1	C-C chemokine receptor 5 [Cercopi...	183	8e-45	
gi 5713092 gb AAD47788.1	C-C chemokine receptor 5 [Erythro...	183	8e-45	
gi 5713091 gb AAD47787.1	C-C chemokine receptor 5 [Mandril...	183	8e-45	
gi 5713070 gb AAD47766.1	C-C chemokine receptor 5 [Lemur c...	183	8e-45	
gi 5713051 gb AAD47747.1	C-C chemokine receptor 5 [Papio p...	183	8e-45	
gi 5713038 gb AAD47734.1	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 5713022 gb AAD47718.1	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 5713019 gb AAD47715.1	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 14582847 gb AAK69684.1	chemokine receptor CCR5 [Cercoceb...	183	8e-45	
gi 2281710 emb CAB02143.1	G PROTEIN-COUPLED RECEPTOR CKR-L...	183	8e-45	G
gi 3135298 gb AAC39831.1	chemokine receptor CCR5 [Cercoceb...	183	8e-45	
gi 433947 emb CAA50673.1	muBLR1 [Mus musculus] >gi 631736 ...	182	1e-44	G
gi 5713084 gb AAD47780.1	C-C chemokine receptor 5 [Cercopi...	182	1e-44	
gi 5713066 gb AAD47762.1	C-C chemokine receptor 5 [Cercopi...	182	1e-44	
gi 3694849 gb AAC62472.1	chemokine receptor CCR5 [Cercoceb...	182	1e-44	
gi 50732852 ref XP_418795.1	PREDICTED: similar to C-C chem...	182	1e-44	G
gi 4406105 gb AAD19859.1	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 4406101 gb AAD19857.1	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 4406097 gb AAD19855.1	C-C chemokine receptor type 5 [Tr...	182	1e-44	
gi 4406095 gb AAD19854.1	C-C chemokine receptor type 5 [Tr...	182	1e-44	
gi 4894984 gb AAD32686.1	CC chemokine receptor 5 [Cercopit...	182	1e-44	
gi 13873077 gb AAK43364.1	C-C chemokine receptor 5 [Colobu...	182	1e-44	
gi 57101678 ref XP_541907.1	PREDICTED: similar to chemokin...	182	1e-44	G
gi 5713074 gb AAD47770.1	C-C chemokine receptor 5 [Saguinus...	182	1e-44	
gi 5713053 gb AAD47749.1	C-C chemokine receptor 5 [Papio p...	182	1e-44	
gi 4406107 gb AAD19860.1	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 5514614 gb AAD44007.1	CC chemokine receptor type 5 [Pan...	182	1e-44	
gi 13873097 gb AAK43374.1	C-C chemokine receptor 5 [Therop...	182	1e-44	
gi 13873079 gb AAK43365.1	C-C chemokine receptor 5 [Nasalis...	182	1e-44	
gi 13873069 gb AAK43360.1	C-C chemokine receptor 5 [Mandri...	182	1e-44	
gi 5713113 gb AAD47809.1	C-C chemokine receptor 5 [Erythro...	182	2e-44	
gi 5713064 gb AAD47760.1	C-C chemokine receptor 5 [Colobus...	182	2e-44	
gi 5713056 gb AAD47752.1	C-C chemokine receptor 5 [Papio p...	182	2e-44	
gi 5713020 gb AAD47716.1	C-C chemokine receptor 5 [Macaca ...	182	2e-44	
gi 5712951 gb AAD47647.1	C-C chemokine receptor 5 [Hylobat...	182	2e-44	
gi 2896820 gb AAC03243.1	chemokine receptor CCR5 [Rattus n...	182	2e-44	G
gi 4894980 gb AAD32684.1	CC chemokine receptor 5 [Colobus ...	182	2e-44	
gi 4426832 gb AAD20560.1	CC chemokine receptor 5 [Gorilla ...	182	2e-44	
gi 13873121 gb AAK43386.1	C-C chemokine receptor 5 [Gorilla ...	182	2e-44	
gi 13873067 gb AAK43359.1	C-C chemokine receptor 5 [Mandri...	182	2e-44	
gi 12407355 gb AAAG53466.1	CC chemokine receptor type 5 [Ce...	182	2e-44	
gi 56553514 gb AAV97929.1	chemokine receptor 5 [Bos taurus...	181	2e-44	G
gi 5713104 gb AAD47800.1	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713096 gb AAD47792.1	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713082 gb AAD47778.1	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713048 gb AAD47744.1	C-C chemokine receptor 5 [Papio p...	181	2e-44	
gi 5713037 gb AAD47733.1	C-C chemokine receptor 5 [Macaca ...	181	2e-44	
gi 5712964 gb AAD47660.1	C-C chemokine receptor 5 [Pan tro...	181	2e-44	
gi 5712949 gb AAD47645.1	C-C chemokine receptor 5 [Hylobat...	181	2e-44	

gi 4426824 gb AAD20552.1	CC chemokine receptor 5 [Macaca a...]	<u>181</u>	2e-44	
gi 4426823 gb AAD20551.1	CC chemokine receptor 5 [Macaca n...]	<u>181</u>	2e-44	
gi 2245620 gb AAB62557.1	CC chemokine receptor-5 [Pan trog...]	<u>181</u>	2e-44	
gi 5713114 gb AAD47810.1	C-C chemokine receptor 5 [Erythro...]	<u>181</u>	3e-44	
gi 5713083 gb AAD47779.1	C-C chemokine receptor 5 [Hylobat...]	<u>181</u>	3e-44	
gi 5713073 gb AAD47769.1	C-C chemokine receptor 5 [Varecia...]	<u>181</u>	3e-44	
gi 5713071 gb AAD47767.1	C-C chemokine receptor 5 [Lemur c...]	<u>181</u>	3e-44	
gi 5713058 gb AAD47754.1	C-C chemokine receptor 5 [Mandril...]	<u>181</u>	3e-44	
gi 5713009 gb AAD47705.1	C-C chemokine receptor 5 [Cercopi...]	<u>181</u>	3e-44	
gi 5712958 gb AAD47654.1	C-C chemokine receptor 5 [Gorilla...]	<u>181</u>	3e-44	
gi 5712955 gb AAD47651.1	C-C chemokine receptor 5 [Gorilla...]	<u>181</u>	3e-44	
gi 16758152 ref NP_445867.1	chemokine (C-X-C motif) recept...	<u>181</u>	3e-44	
gi 4406113 gb AAD19863.1	C-C chemokine receptor type 5 [Hy...]	<u>181</u>	3e-44	
gi 4406103 gb AAD19858.1	C-C chemokine receptor type 5 [Po...]	<u>181</u>	3e-44	
gi 13873113 gb AAK43382.1	C-C chemokine receptor 5 [Hyloba...]	<u>181</u>	3e-44	
gi 13873083 gb AAK43367.1	C-C chemokine receptor 5 [Hyloba...]	<u>181</u>	3e-44	
gi 9502106 gb AAF87982.1	CC chemokine receptor 5 [Cercopit...]	<u>181</u>	3e-44	
gi 5713093 gb AAD47789.1	C-C chemokine receptor 5 [Erythro...]	<u>181</u>	4e-44	
gi 5713085 gb AAD47781.1	C-C chemokine receptor 5 [Cercopi...]	<u>181</u>	4e-44	
gi 5713072 gb AAD47768.1	C-C chemokine receptor 5 [Varecia...]	<u>181</u>	4e-44	
gi 5713055 gb AAD47751.1	C-C chemokine receptor 5 [Papio p...]	<u>181</u>	4e-44	
gi 5713042 gb AAD47738.1	C-C chemokine receptor 5 [Macaca ...]	<u>181</u>	4e-44	
gi 5713034 gb AAD47730.1	C-C chemokine receptor 5 [Macaca ...]	<u>181</u>	4e-44	
gi 5514616 gb AAD44009.1	CC chemokine receptor type 5 [Cer...]	<u>181</u>	4e-44	
gi 13873081 gb AAK43366.1	C-C chemokine receptor 5 [Trachy...]	<u>181</u>	4e-44	
gi 9502104 gb AAF87981.1	CC chemokine receptor 5 [Hylobate...]	<u>181</u>	4e-44	
gi 4757938 ref NP_000639.1	chemokine (C-C motif) receptor ...	<u>180</u>	5e-44	
gi 57113969 ref NP_001009046.1	chemokine (C-C motif) recep...	<u>180</u>	5e-44	
gi 5713079 gb AAD47775.1	C-C chemokine receptor 5 [Cercopi...]	<u>180</u>	5e-44	
gi 5712968 gb AAD47664.1	C-C chemokine receptor 5 [Pongo p...]	<u>180</u>	5e-44	
gi 5712966 gb AAD47662.1	C-C chemokine receptor 5 [Pan tro...]	<u>180</u>	5e-44	
gi 5712961 gb AAD47657.1	C-C chemokine receptor 5 [Pan tro...]	<u>180</u>	5e-44	
gi 5712960 gb AAD47656.1	C-C chemokine receptor 5 [Pan tro...]	<u>180</u>	5e-44	
gi 48675899 ref NP_001001618.1	chemokine C-C motif recepto...	<u>180</u>	5e-44	
gi 23193462 gb AAN14531.1	chemokine receptor CCR5 [Saimiri...]	<u>180</u>	5e-44	
gi 2305120 gb AAB65701.1	CCR5 receptor [Homo sapiens]	<u>180</u>	5e-44	
gi 4502633 ref NP_000638.1	chemokine (C-C motif) receptor ...	<u>180</u>	7e-44	
gi 5713002 gb AAD47698.1	C-C chemokine receptor 5 [Callith...]	<u>180</u>	7e-44	
gi 51592090 ref NP_446412.2	chemokine (C-C) receptor 5 [Ra...]	<u>180</u>	7e-44	
gi 54038473 gb AAR84427.1	CXCR2 protein [Xenopus laevis] >...	<u>180</u>	7e-44	
gi 57898982 dbj BAD86855.1	CXC chemokine receptor 3 [Canis...	<u>180</u>	7e-44	
gi 3135296 gb AAC39830.1	chemokine receptor CCR5 [Cercoceb...]	<u>180</u>	7e-44	
gi 47208340 emb CAF88488.1	unnamed protein product [Tetrao...]	<u>180</u>	7e-44	
gi 90075 pir JQ1231	interleukin-8 receptor - rabbit >gi 12...	<u>179</u>	9e-44	
gi 5713054 gb AAD47750.1	C-C chemokine receptor 5 [Papio p...]	<u>179</u>	9e-44	
gi 5712977 gb AAD47673.1	C-C chemokine receptor 5 [Homo sa...]	<u>179</u>	9e-44	
gi 42540827 gb AAS19314.1	CCR5 chemokine receptor [Homo sa...]	<u>179</u>	9e-44	
gi 3694853 gb AAC62474.1	chemokine receptor CCR5 [Cercoceb...]	<u>179</u>	9e-44	
gi 2305132 gb AAB65707.1	CCR5 receptor [Homo sapiens]	<u>179</u>	9e-44	
gi 3135300 gb AAC39832.1	chemokine receptor CCR5 [Cercoceb...]	<u>179</u>	9e-44	
gi 6753466 ref NP_034045.1	chemokine (C-C motif) receptor ...	<u>179</u>	1e-43	
gi 57086223 ref XP_546496.1	PREDICTED: similar to Burkitt ...	<u>179</u>	1e-43	
gi 5712982 gb AAD47678.1	C-C chemokine receptor 5 [Homo sa...]	<u>179</u>	1e-43	
gi 5712969 gb AAD47665.1	C-C chemokine receptor 5 [Pongo p...]	<u>179</u>	1e-43	

gi 5712963 gb AAD47659.1	C-C chemokine receptor 5 [Pan tro...	179	1e-43	
gi 3694851 gb AAC62473.1	chemokine receptor CCR5 [Cercoceb...	179	1e-43	
gi 631602 pir A53752	interleukin-8 receptor (clone 5B1a) -...	179	1e-43	
gi 29169293 gb AAO65971.1	chemokine receptor 5 [Homo sapie...	179	1e-43	G
gi 16758000 ref NP_445755.1	Burkitt lymphoma receptor 1 [R...	179	1e-43	G
gi 5713087 gb AAD47783.1	C-C chemokine receptor 5 [Alouatt...	179	1e-43	
gi 5713008 gb AAD47704.1	C-C chemokine receptor 5 [Cercopi...	179	1e-43	
gi 5713003 gb AAD47699.1	C-C chemokine receptor 5 [Callith...	179	1e-43	
gi 5712981 gb AAD47677.1	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 5712976 gb AAD47672.1	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 5712974 gb AAD47670.1	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 42540823 gb AAS19312.1	CCR5 chemokine receptor [Homo sa...	179	1e-43	G
gi 4337456 gb AAD18131.1	chemokine receptor 5 [Homo sapiens]	179	1e-43	G
gi 2305190 gb AAB65736.1	CCR5 receptor [Homo sapiens] >gi ...	179	1e-43	G
gi 2305180 gb AAB65731.1	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305168 gb AAB65725.1	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305156 gb AAB65719.1	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305142 gb AAB65712.1	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305128 gb AAB65705.1	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 58760247 gb AAW82038.1	CC chemokine receptor 5 variant ...	179	1e-43	
gi 4206191 gb AAD11572.1	chemokine receptor [Macaca mulatt...	179	1e-43	
gi 4200299 emb CAA08838.1	CCR5 chemokine receptor [Felis c...	179	1e-43	G
gi 1321935 emb CAA62563.1	interleukin-8 receptor type B [P...	179	1e-43	
gi 5712980 gb AAD47676.1	C-C chemokine receptor 5 [Homo sa...	178	2e-43	G
gi 2305200 gb AAB65741.1	CCR5 receptor [Pan troglodytes]	178	2e-43	G
gi 2305196 gb AAB65739.1	CCR5 receptor [Pan troglodytes]	178	2e-43	G
gi 58760249 gb AAW82039.1	CC chemokine receptor 5 variant ...	178	2e-43	
gi 23305852 gb AAN17315.1	interleukin 8 receptor B CXCR2 [...]	178	3e-43	
gi 27805835 ref NP_776726.1	chemokine (C-X-C motif) recept...	178	3e-43	G
gi 4504683 ref NP_001548.1	interleukin 8 receptor beta [Ho...	178	3e-43	G
gi 2305176 gb AAB65729.1	CCR5 receptor [Homo sapiens]	178	3e-43	G
gi 2305136 gb AAB65709.1	CCR5 receptor [Homo sapiens]	178	3e-43	G
gi 57163789 ref NP_001009248.1	chemokine receptor 5 [Felis...	177	3e-43	G
gi 5713005 gb AAD47701.1	C-C chemokine receptor 5 [Alouatt...	177	3e-43	
gi 5712975 gb AAD47671.1	C-C chemokine receptor 5 [Homo sa...	177	3e-43	G
gi 2305178 gb AAB65730.1	CCR5 receptor [Homo sapiens]	177	3e-43	G
gi 13873089 gb AAK43370.1	C-C chemokine receptor 5 [Callic...	177	3e-43	
gi 13873075 gb AAK43363.1	C-C chemokine receptor 5 [Alouat...	177	3e-43	
gi 5713080 gb AAD47776.1	C-C chemokine receptor 5 [Callith...	177	4e-43	
gi 23193460 gb AAN14530.1	chemokine receptor CCR5 [Callith...	177	4e-43	
gi 33521604 gb AAQ20014.1	CC chemokine receptor 5 [Callith...	177	4e-43	
gi 2305158 gb AAB65720.1	CCR5 receptor [Homo sapiens]	177	4e-43	G
gi 1935045 gb AAB51765.1	fusin [Felis catus]	177	4e-43	G
gi 9502108 gb AAF87983.1	CC chemokine receptor 5 [Lagothri...	177	4e-43	
gi 5712948 gb AAD47644.1	C-C chemokine receptor 5 [Hylobat...	177	6e-43	
gi 33521602 gb AAQ20013.1	CC chemokine receptor 5 [Callith...	177	6e-43	
gi 2305148 gb AAB65715.1	CCR5 receptor [Homo sapiens]	177	6e-43	G
gi 13873083 gb AAK43368.1	C-C chemokine receptor 5 [Ateles...	177	6e-43	
gi 2347114 gb AAC53386.1	CC chemokine receptor-5 [Mus musc...	177	6e-43	G
gi 1237134 gb AAC52453.1	JE receptor	176	7e-43	G

gi 57100809 ref XP_541020.1	PREDICTED: hypothetical protein	176	7e-43	G
gi 2896818 gb AAC03242.1	chemokine receptor CCR2 [Rattus norvegicus]	176	7e-43	G
gi 58760245 gb AAW82037.1	CC chemokine receptor 5 variant	176	1e-42	
gi 58652135 ref NP_001011675.1	Burkitt lymphoma receptor 1	176	1e-42	G
gi 6002764 gb AAF00130.1	chemokine receptor CXCR4-Lo [Homo sapiens]	176	1e-42	G
gi 33521612 gb AAQ20018.1	CC chemokine receptor 5 [Leontopithecus rosalia]	176	1e-42	
gi 33521606 gb AAQ20015.1	CC chemokine receptor 5 [Leontopithecus rosalia]	176	1e-42	
gi 2305124 gb AAB65703.1	CCR5 receptor [Homo sapiens]	176	1e-42	G
gi 60097918 ref NP_001012342.2	chemokine (C-C motif) receptor	176	1e-42	
gi 1842247 gb AAC48852.1	CXCR-4 homolog [Felis catus] >gi 1842247 gb AAC48852.1	176	1e-42	G
gi 3059120 emb CAA12166.1	CXCR4 [Homo sapiens]	176	1e-42	G
gi 2305140 gb AAB65711.1	CCR5 receptor [Homo sapiens]	175	2e-42	G
gi 3243095 gb AAC23950.1	putative chemokine receptor [Gallus gallus]	175	2e-42	
gi 9502112 gb AAF87985.1	CC chemokine receptor 5 [Ateles sp.]	175	2e-42	
gi 5713007 gb AAD47703.1	C-C chemokine receptor 5 [Actus tenuis]	175	2e-42	
gi 47523298 ref NP_998938.1	chemokine (C-X-C motif) receptor	175	2e-42	G
gi 23305854 gb AAN17316.1	interleukin 8 receptor B CXCR2 [Mus musculus]	175	2e-42	
gi 33521616 gb AAQ20020.1	CC chemokine receptor 5 [Brachytarsomys tarsalis]	175	2e-42	
gi 2431976 gb AAB71183.1	CCR5 [Mus musculus]	175	2e-42	G
gi 57113963 ref NP_001009047.1	chemokine (C-X-C motif) receptor	174	3e-42	G
gi 42540825 gb AAS19313.1	CCR5 chemokine receptor [Homo sapiens]	174	3e-42	G
gi 30584919 gb AAP36716.1	Homo sapiens chemokine (C-X-C motif)	174	3e-42	
gi 33521610 gb AAQ20017.1	CC chemokine receptor 5 [Leontopithecus rosalia]	174	3e-42	
gi 49118568 gb AAH73571.1	LOC443669 protein [Xenopus laevis]	174	3e-42	G
gi 2305166 gb AAB65724.1	CCR5 receptor [Homo sapiens]	174	3e-42	G
gi 4100052 gb AAD00729.1	CCR5 [Felis catus]	174	3e-42	G
gi 1698716 gb AAB37273.1	beta chemokine receptor [Mus musculus]	174	3e-42	G
gi 1321889 emb CAA62565.1	interleukin-8 receptor type B [Mus musculus]	174	3e-42	
gi 9587720 gb AAF89352.1	chemokine receptor CXCR4 [Gorilla gorilla]	174	3e-42	
gi 9587716 gb AAF89350.1	chemokine receptor CXCR4 [Hylobates lar]	174	3e-42	
gi 13549090 gb AAK29630.1	chemokine receptor CXCR4 [Homo sapiens]	174	4e-42	G
gi 9587714 gb AAF89349.1	chemokine receptor CXCR4 [Hylobates lar]	174	4e-42	
gi 57111005 ref XP_536064.1	PREDICTED: similar to interleukin-8 receptor	174	5e-42	G
gi 5712979 gb AAD47675.1	C-C chemokine receptor 5 [Homo sapiens]	174	5e-42	G
gi 33521614 gb AAQ20019.1	CC chemokine receptor 5 [Leontopithecus rosalia]	174	5e-42	
gi 1321816 emb CAA62564.1	interleukin-8 receptor type B [Gallus gallus]	174	5e-42	
gi 9587724 gb AAF89354.1	chemokine receptor CXCR4 [Ateles sp.]	174	5e-42	
gi 35187401 gb AAQ84305.1	CXC chemokine receptor 1-like protein	173	6e-42	G
gi 5712985 gb AAD47681.1	C-C chemokine receptor 5 [Saguinus oedipus]	173	6e-42	
gi 31044501 gb AAQ47588.2	chemokine receptor CXCR4 [Tupaia belangeri]	173	6e-42	
gi 2305192 gb AAB65737.1	CCR5 receptor [Homo sapiens]	173	6e-42	G
gi 5712992 gb AAD47688.1	C-C chemokine receptor 5 [Saguinus oedipus]	173	8e-42	
gi 33521608 gb AAQ20016.1	CC chemokine receptor 5 [Leontopithecus rosalia]	173	8e-42	
gi 57157736 dbj BAD83840.1	CC chemokine receptor 5 [Canis lupus]	173	8e-42	G
gi 9587722 gb AAF89353.1	chemokine receptor CXCR4 [Alouatta palliata]	173	8e-42	
gi 2851566 sp P51682 CKRS_MOUSE	C-C chemokine receptor type 5	173	8e-42	G
gi 57101676 ref XP_541906.1	PREDICTED: similar to chemokine receptor	172	1e-41	G
gi 5712990 gb AAD47686.1	C-C chemokine receptor 5 [Saguinus oedipus]	172	1e-41	
gi 5712983 gb AAD47679.1	C-C chemokine receptor 5 [Saguinus oedipus]	172	1e-41	
gi 23193458 gb AAN14529.1	chemokine receptor CXCR4 [Saimiri sciureus]	172	1e-41	
gi 9587732 gb AAF89358.1	chemokine receptor CXCR4 [Pithecius satzingeri]	172	1e-41	
gi 31542356 ref NP_034047.2	chemokine (C-C motif) receptor	172	1e-41	G

gi 23193456 gb AAN14528.1	chemokine receptor CXCR4 [Callit...]	172	1e-41	
gi 13430095 gb AAK25743.1	chemokine receptor CXCR4 [Macaca...]	172	1e-41	
gi 2625094 gb AAC63831.1	CXC chemokine receptor 4 [Papio c...]	172	1e-41	
gi 4467415 emb CAB37671.1	interleukin-8 receptor type A [G...]	172	1e-41	
gi 9587730 gb AAF89357.1	chemokine receptor CXCR4 [Callice...]	172	1e-41	
gi 9587696 gb AAF89340.1	chemokine receptor CXCR4 [Presbyt...]	172	1e-41	
gi 42557658 emb CAF28777.1	C-C chemokine receptor 5 like [...]	172	2e-41	
gi 6318165 emb CAB60252.1	CXC chemokine receptor 4 [Acipen...]	172	2e-41	
gi 8393600 ref NP_058879.1	interleukin 8 receptor, beta [R...]	172	2e-41	G
gi 50732854 ref XP_418796.1	PREDICTED: similar to C-C chem...	171	2e-41	G
gi 17902281 gb AAL47855.1	chemokine receptor CXCR4 [Rattus...]	171	2e-41	G
gi 1419629 emb CAA63867.1	MIP-1 alpha receptor [Mus musculus]	171	2e-41	G
gi 3294342 dbj BAA31327.1	CXCR4 receptor [Cercopithecus ae...]	171	2e-41	
gi 9587698 gb AAF89341.1	chemokine receptor CXCR4 [Mandril...]	171	2e-41	
gi 9587690 gb AAF89337.1	chemokine receptor CXCR4 [Presbyt...]	171	2e-41	
gi 5713006 gb AAD47702.1	C-C chemokine receptor 5 [Actus t...]	171	3e-41	
gi 5712988 gb AAD47684.1	C-C chemokine receptor 5 [Saguinus...]	171	3e-41	
gi 48675907 ref NP_001001619.1	chemokine C-C motif recepto...	171	3e-41	G
gi 4102992 gb AAD01638.1	G-protein coupled receptor; CXCR4...	171	3e-41	
gi 12911294 gb AAC39641.1	alpha-chemokine receptor 4 [Macac...]	171	3e-41	
gi 1906613 gb AAB50408.1	CXC chemokine receptor [Rattus no...]	171	3e-41	G
gi 9587708 gb AAF89346.1	chemokine receptor CXCR4 [Macaca ...]	171	3e-41	
gi 9587700 gb AAF89342.1	chemokine receptor CXCR4 [Mandril...]	171	3e-41	
gi 298783 gb AAB25879.1	interleukin-8 receptor type 1, IL8...	171	4e-41	G
gi 5712989 gb AAD47685.1	C-C chemokine receptor 5 [Saguinus...]	171	4e-41	
gi 7230482 gb AAF42991.1	CXC chemokine receptor 4 [Hylobat...]	171	4e-41	
gi 9587688 gb AAF89336.1	chemokine receptor CXCR4 [Presbyt...]	171	4e-41	
gi 5712993 gb AAD47689.1	C-C chemokine receptor 5 [Saguinus...]	170	5e-41	
gi 1899056 gb AAC51159.1	CXCR4 gene product [Macaca mulatt...]	170	5e-41	
gi 9587728 gb AAF89356.1	chemokine receptor CXCR4 [Callimi...]	170	5e-41	
gi 57163985 ref NP_001009241.1	chemokine (C-C motif) recep...	170	7e-41	G
gi 9506809 ref NP_062183.1	interleukin 8 receptor, alpha [...]	170	7e-41	G
gi 27805943 ref NP_776785.1	interleukin 8 receptor, beta [...]	170	7e-41	G
gi 23305862 gb AAN17320.1	interleukin 8 receptor B CXCR2 [...]	170	7e-41	
gi 7141318 gb AAF37288.1	CXCR4 receptor [Saimiri boliviensis]	170	7e-41	
gi 9587726 gb AAF89355.1	chemokine receptor CXCR4 [Callith...]	170	7e-41	
gi 4502631 ref NP_001286.1	chemokine (C-C motif) receptor ...	169	9e-41	G
gi 5712994 gb AAD47690.1	C-C chemokine receptor 5 [Saguinus...]	169	9e-41	
gi 23305858 gb AAN17318.1	interleukin 8 receptor B CXCR2 [...]	169	9e-41	
gi 219863 dbj BAA01723.1	HM145 [Homo sapiens]	169	9e-41	G
gi 7441609 pir G00048	fusin (LESTRA) - crab-eating macaque...	169	9e-41	
gi 9587738 gb AAF89361.1	chemokine receptor CXCR4 [Nyctice...]	169	9e-41	
gi 1237136 gb AAC52454.1	MIP-1 alpha receptor	169	1e-40	G
gi 4504681 ref NP_000625.1	interleukin 8 receptor alpha [H...]	169	1e-40	G
gi 27802639 gb AAO21209.1	chemokine receptor CXCR4 [Petrom...]	169	1e-40	
gi 20380431 gb AAB28221.1	Interleukin 8 receptor alpha [Ho...]	169	1e-40	G
gi 1934671 gb AAB54116.1	alpha chemokine receptor [Macaca ...]	169	1e-40	
gi 4467981 emb CAB37850.1	interleukin-8 receptor type A [P...]	169	1e-40	
gi 55741694 ref NP_001003151.1	interleukin-8 receptor [Can...]	169	2e-40	G
gi 10120494 ref NP_065417.1	macrophage inflammatory protein...	169	2e-40	G
gi 45382915 ref NP_989948.1	chemokine receptor CXCR4 [Gall...]	169	2e-40	G
gi 3135304 gb AAC39834.1	chemokine receptor CXCR4 [Cercoce...]	169	2e-40	
gi 7108519 gb AAF36453.1	chemokine receptor [Callithrix ja...]	169	2e-40	
gi 48675909 ref NP_001001621.1	chemokine C-C motif recepto...	168	2e-40	G

gi 11024708 ref NP_031747.2	G protein-coupled receptor 2 [...]	168	3e-40	G
gi 48735085 gb AAH72397.1	Interleukin 8 receptor alpha [Homo...]	168	3e-40	G
gi 34873846 ref XP_343969.1	similar to 7-transmembrane G-p...	167	3e-40	G
gi 55616095 ref XP_526027.1	PREDICTED: similar to High aff...	167	3e-40	G
gi 23305856 gb AAN17317.1	interleukin 8 receptor B CXCR2 [...]	167	3e-40	
gi 2305126 gb AAB65704.1	CCR5 receptor [Homo sapiens]	167	3e-40	G
gi 7230484 gb AAF42992.1	CXC chemokine receptor 4 [Saguinus...]	167	3e-40	
gi 7230480 gb AAF42990.1	CXC chemokine receptor 4 [Cercopit...	167	3e-40	
gi 9587740 gb AAF89362.1	chemokine receptor CXCR4 [Eulemur...	167	3e-40	
gi 7108517 gb AAF36452.1	chemokine receptor [Oryctolagus c...	167	4e-40	
gi 6753456 ref NP_034039.1	interleukin 8 receptor beta [Mu...]	167	6e-40	G
gi 6753460 ref NP_034041.1	chemokine (C-X-C motif) recepto...	167	6e-40	G
gi 29602789 gb AAO84922.1	interleukin-8 receptor CXCR2 [Ca...	167	6e-40	
gi 17223091 gb AAL18011.1	Cxcr4A [Danio rerio]	167	6e-40	G
gi 7546849 gb AAE63711.1	CC chemokine receptor 10B [Mus mu...]	167	6e-40	G
gi 7546847 gb AAE63710.1	CC chemokine receptor 10A [Mus mu...]	167	6e-40	G
gi 1542889 emb CAB02202.1	CXCR-4 [Mus musculus]	167	6e-40	G
gi 543400 pir S42096	interleukin-8 receptor - rat	167	6e-40	
gi 1666649 emb CAA67894.1	leukocyte-derived seven transmem...	166	8e-40	G
gi 9587742 gb AAF89363.1	chemokine receptor CXCR4 [Perodic...	166	8e-40	
gi 57091477 ref XP_548084.1	PREDICTED: similar to hypothet...	166	1e-39	G
gi 38016879 gb AAR07898.1	CC chemokine receptor 10 [Homo s...]	165	2e-39	G
gi 23305860 gb AAN17319.1	interleukin 8 receptor B CXCR2 [...]	165	2e-39	
gi 47215024 emb CAG01842.1	unnamed protein product [Tetrao...	165	2e-39	
gi 34223272 gb AAO66450.1	CXCR4 [Macaca fascicularis] >gi ...	163	6e-39	
gi 40254673 ref NP_571957.2	chemokine (C-X-C motif) recepto...	163	6e-39	G
gi 5712991 gb AAD47687.1	C-C chemokine receptor 5 [Saguinus...]	163	8e-39	
gi 55250561 gb AAH85659.1	Zgc:92301 [Danio rerio] >gi 5592...	162	1e-38	G
gi 52546730 ref NP_001005261.1	C-C chemokine receptor 3 [C...	162	1e-38	G
gi 55620263 ref XP_526193.1	PREDICTED: CC chemokine recept...	162	1e-38	G
gi 50732904 ref XP_418820.1	PREDICTED: similar to CX3C che...	162	1e-38	G
gi 47212519 emb CAF98051.1	unnamed protein product [Tetrao...	162	1e-38	
gi 9628081 ref NP_042675.1	G protein-coupled receptor [Equ...	162	2e-38	G
gi 37655185 gb AAO65970.2	chemokine receptor 3 [Homo sapie...	162	2e-38	G
gi 42557657 emb CAF28776.1	C-C chemokine receptor 11 like ...	162	2e-38	
gi 2137554 pir I49341	MIP-1 alpha receptor like-2 - mouse	161	2e-38	
gi 7705316 ref NP_057686.1	CC chemokine receptor 10 [Homo ...]	161	2e-38	G
gi 52138984 gb AAH82709.1	LOC494705 protein [Xenopus laevis]	161	2e-38	G
gi 1203801 gb AAA89155.1	MIP-1 alpha receptor like-2	161	2e-38	G
gi 3551197 gb BAA32797.1	CXCR4 [Cyprinus carpio]	161	2e-38	
gi 577415 gb AAA64593.1	G protein-coupled receptor	161	3e-38	G
gi 1109784 gb AAA86118.1	chemokine G-protein-coupled recep...	161	3e-38	G
gi 48675903 ref NP_001001620.1	chemokine C-C motif recepto...	161	3e-38	G
gi 57157738 gb BAD83841.1	CC chemokine receptor 3 [Canis ...]	160	4e-38	G
gi 1477561 gb AAB09726.1	C-C chemokine receptor 3 >gi 7441...	160	4e-38	G
gi 1082383 pir R55733	G protein-coupled receptor GPR2 - hu...	160	5e-38	
gi 22074362 gb AAL13085.1	eotaxin receptor [Mus musculus] ...	159	9e-38	G
gi 15029747 gb AAH11092.1	Chemokine (C-C motif) receptor 1...	159	9e-38	G
gi 27721857 ref XP_236742.1	similar to MIP-1 alpha recepto...	159	9e-38	G

gi 27924174 gb AAH44963.1	Cxcr4-prov protein [Xenopus laevis]	159	1e-37	G
gi 31542352 ref NP_034042.2	chemokine (C-C motif) receptor...	159	1e-37	G
gi 49115863 gb AAH73603.1	Unknown (protein for MGC:82907) ...	159	1e-37	
gi 8118035 gb AAF72671.1	7-transmembrane G-protein coupled...	159	1e-37	G
gi 3327018 emb CAA04493.1	CXC chemokine receptor [Oncorhyn...	159	2e-37	
gi 47220226 emb CAF98991.1	unnamed protein product [Tetrao...	159	2e-37	
gi 26327025 dbj BAC27256.1	unnamed protein product [Mus mu...	159	2e-37	G
gi 881548 gb AAA89153.1	macrophage inflammatory protein-1 ...	158	2e-37	G
gi 1109786 gb AAA86119.1	chemokine G-protein-coupled recep...	158	2e-37	G
gi 2407217 gb AAB70526.1	chemokine receptor [Macaca mulatt...	158	2e-37	
gi 31542354 ref NP_034044.2	CC chemokine receptor 3 [Mus m...	157	4e-37	G
gi 50732143 ref XP_418499.1	PREDICTED: similar to CC-chemo...	157	5e-37	G
gi 6467133 dbj BAA86964.1	b-chemokine receptor CCR3 [Homo ...	157	6e-37	G
gi 16758844 ref NP_446410.1	CC chemokine receptor 3 [Rattu...	156	8e-37	G
gi 50540418 ref NP_001002675.1	zgc:91924 [Danio rerio] >gi...	156	1e-36	G
gi 18858507 ref NP_571909.1	chemokine (C-X-C motif), recep...	156	1e-36	G
gi 3930519 gb AAC80428.1	C-C chemokine receptor 3 [Cavia p...	156	1e-36	
gi 2897073 gb AAC03337.1	chemokine receptor CCR3 [Rattus n...	155	2e-36	G
gi 13929467 ref NP_001287.2	chemokine binding protein 2 [H...	154	4e-36	G
gi 30583827 gb AAP36162.1	Homo sapiens chemokine binding p...	154	4e-36	
gi 30171328 gb AAP20651.1	chemokine-binding protein 2 [Hom...	154	4e-36	G
gi 2213809 gb AAB97728.1	CC-chemokine-binding receptor JAB...	154	5e-36	G
gi 51870077 ref YP_073630.1	Hypothetical protein LDVICp124...	153	7e-36	G
gi 2266686 emb CAA74107.1	C-C chemokine receptor-3 [Macaca...	153	7e-36	
gi 2266434 emb CAA74106.1	C-C chemokine receptor-3 [Cercop...	153	9e-36	
gi 4885121 ref NP_005192.1	chemokine (C-C motif) receptor ...	152	1e-35	G
gi 55620239 ref XP_526178.1	PREDICTED: chemokine (C-C moti...	152	1e-35	G
gi 30962608 gb AAP42156.1	chemokine receptor D6 [Homo sapi...	152	1e-35	G
gi 42597659 emb CAF28778.1	C-C chemokine receptor 8 like [...	152	1e-35	
gi 22652109 gb AAN03618.1	eotaxin receptor CCR3 [Macaca mu...	152	1e-35	
gi 22652103 gb AAN03615.1	eotaxin receptor CCR3 [Macaca fa...	152	1e-35	
gi 18071641 gb AAL55443.1	chemokine receptor 3 [Macaca fas...	152	1e-35	
gi 18071639 gb AAL55442.1	chemokine receptor 3 [Macaca fas...	152	1e-35	
gi 13027670 gb AAK08628.1	CC chemokine receptor 8 [Homo sa...	152	1e-35	G
gi 2407219 gb AAB70527.1	chemokine receptor [Macaca mulatt...	152	2e-35	
gi 6671770 ref NP_031744.1	chemokine (C-C motif) receptor ...	151	3e-35	G
gi 57103782 ref XP_542719.1	PREDICTED: similar to chemokin...	150	4e-35	G
gi 47220980 emb CAF98209.1	unnamed protein product [Tetrao...	150	4e-35	
gi 3298340 dbj BAA31458.1	CXC chemokine receptor-1 [Cyprin...	150	4e-35	
gi 347190 gb AAC37873.1	G protein-coupled receptor >gi 586...	150	6e-35	
gi 18448639 gb AAL69885.1	SPV146 G protein-coupled CC chem...	150	6e-35	G
gi 13430087 gb AAK25739.1	chemokine receptor CCR3 [Macaca ...	150	6e-35	
gi 34740123 dbj BAC87713.1	C-C chemokine receptor-3 [Paral...	149	2e-34	
gi 31542483 ref NP_067622.2	D6 beta-chemokine receptor [Mu...	147	4e-34	G
gi 3851699 gb AAC72403.1	chemokine receptor [Macaca mulatt...	147	4e-34	
gi 55562725 gb AAH86449.1	Chemokine binding protein 2 [Rat...	147	6e-34	G
gi 57103810 ref XP_542737.1	PREDICTED: similar to chemokin...	146	8e-34	G
gi 13897910 gb AAK48497.1	IL-8 receptor [Oncorhynchus mykiss]	145	2e-33	
gi 13897920 gb AAK48502.1	IL-8 receptor [Oncorhynchus mykiss]	145	2e-33	
gi 2213807 gb AAB61572.1	CC-chemokine-binding receptor JAB...	145	2e-33	G

<u>gi 2072651 emb CAA73379.1 </u>	beta-chemokine receptor D6 [Mus ...	<u>144</u>	3e-33	
<u>gi 47227892 emb CAG09055.1 </u>	unnamed protein product [Tetrao...	<u>144</u>	5e-33	
<u>gi 109222 pir A23669 </u>	interleukin-8 receptor, high affinity...	<u>143</u>	7e-33	
<u>gi 27721715 ref XP_236704.1 </u>	similar to chemokine receptor ...	<u>142</u>	1e-32	
<u>gi 54038607 gb AAH84447.1 </u>	Hypothetical LOC496477 [Xenopus ...	<u>142</u>	2e-32	
<u>gi 1354505 gb AAB01981.1 </u>	chemokine receptor LCR1 [Rattus n...	<u>141</u>	3e-32	
<u>gi 3298358 dbj BAA31470.1 </u>	CXC chemokine receptor-2 [Cyprin...	<u>141</u>	3e-32	
<u>gi 19424190 ref NP_598218.1 </u>	Rbs11 protein [Rattus norvegic...	<u>140</u>	5e-32	
<u>gi 13897918 gb AAK48501.1 </u>	IL-8 receptor [Oncorhynchus myki...	<u>140</u>	5e-32	
<u>gi 15215068 gb AAH12653.1 </u>	Chemokine (C-X3-C) receptor 1 [M...	<u>140</u>	8e-32	
<u>gi 26331012 dbj BAC29236.1 </u>	unnamed protein product [Mus mu...	<u>140</u>	8e-32	

Alignments

Get selected sequences Select all Deselect all

>gi|422826|pir||A45680| G protein-coupled peptide receptor EBI 1 - human
gi|183485|gb|AAA58615.1|  EBV induced G-protein coupled receptor
Length = 378

Score = 688 bits (1775), Expect = 0.0
Identities = 351/378 (92%), Positives = 351/378 (92%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF

Sbjct: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXTYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
LPIMYSIICF TYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAK

Sbjct: 61 LPIMYSIICFVGLLNGLVLTYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV
Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180

Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240
GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS
Sbjct: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240

Query: 241 FCYLVIIRTLQARNFERXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
FCYLVIIRTLQARNFERN QLPYNGVVLAQTVANFNITSSTCEL
Sbjct: 241 FCYLVIIRTLQARNFERNKAIKVIIAVVVFIVFQLPYNGVVLAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKD LGCLSQEQLRQWSSCRH 360
SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKD LGCLSQEQLRQWSSCRH
Sbjct: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKD LGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTFSP 378
IRRSSMSVEAETTTFSP
Sbjct: 361 IRRSSMSVEAETTTFSP 378

► gi|4502641|ref|NP_001829.1| G chemokine (C-C motif) receptor 7 precursor [Homo sapiens]
gi|23243434|gb|AAH35343.1| G Chemokine (C-C motif) receptor 7, precursor [Homo sapiens]
gi|49176610|gb|AAT52232.1| G CC chemokine receptor 7 [Homo sapiens]
gi|468316|gb|AAA74230.1| G G protein-coupled receptor [Homo sapiens]
gi|1082381|pir|B55735 lymphocyte-specific G protein-coupled receptor EBI1 - human
gi|468320|gb|AAA74231.1| G G protein-coupled receptor
gi|1352335|sp|P32248|CKR7_HUMAN G C-C chemokine receptor type 7 precursor (C-C CKR7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1) (EBI1) (BLR2)
Length = 378

Score = 682 bits (1760), Expect = 0.0
Identities = 348/378 (92%), Positives = 349/378 (92%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF
Sbjct: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSII~~C~~XXXXXXXXXXXXXXTYIYFKRLKTM~~T~~DTY~~L~~LNLA~~V~~ADIL~~F~~LL~~T~~LPFWAYSAAK 120
LPIMYSII~~C~~ TYIYFKRLKTM~~T~~DTY~~L~~LNLA~~V~~ADIL~~F~~LL~~T~~LPFWAYSAAK
Sbjct: 61 LPIMYSII~~C~~FVG~~L~~LNGLVVL~~T~~IYFKRLKTM~~T~~DTY~~L~~LNLA~~V~~ADIL~~F~~LL~~T~~LPFWAYSAAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
SWVFGVHFCKLIFAIYKMSFFSGMLLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCV
Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180

Query: 181 GSAILLATVLSIPELLYSDLORSSSEOAMRC5LITEHVEAFITIOVAOMVIGFLVPLIAMS 240

G I L A T V L S I P E L L Y S D L Q R S S S E Q A M R C S L I T E H V E A F I T I Q V A Q M V I G F L V P L A M S

Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
FCYLVIIRTLQARNFERN QL PYNGVVL AQTVANFNITSSTCEL

Subjct: 241 FCYLVIIIRTLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAVDTVYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360

Sbjct: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRH 360
Query: 361 IRRSSMSVEAETTTTFSP 378

Sbjct: 361 IRRSSSMSVEAETTTTFSP 378

gi|31127005|qb|AAN47099.2| CC chemokine receptor 7 [Macaca mulatta]
Length = 378

Score = 675 bits (1742), Expect = 0.0
Identities = 346/378 (91%), Positives = 347/378 (91%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTDYTLFESLCSKKDVRNFKAWF 60
MDLGKPMKSVLVALLVIFQV LCQDEVTDDYIGDNTTDYTLFESLCSKKDVRNFKAWF
Sbjct: 1 MDLGKPMKSVLVALLVIFQVYLCQDEVTDDYIGDNTTDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXXTIYFKRLKTMTDTYLLNLAVADILFLTLTLPFWAYSAAK 120
LPIMYSIICF . TYIYFKRLKTMTDTYLLNLAVADILFLTLTLPFWAYSAAK
Sbjct: 61 LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDTYLLNLAVADILFLTLTLPFWAYSAAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV
 Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180

Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240
 G ILATVLSIPELLYSLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS
 Sbjct: 181 GIWILATVLSIPELLYSGLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240

Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSSTCEL 300
 FCYLVIIRTLQARNFERN QLPYNGVVLAAQTVANFNITSSTCEL
 Sbjct: 241 FCYLVIIRTLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKD LGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRND+FKLFKD LGCLSQEQLRQWSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDLFKLFKD LGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 IRRSSMSVEAETTTTFSP
 Sbjct: 361 IRRSSMSVEAETTTTFSP 378

 >gi|55645367|ref|XP_511477.1|  PREDICTED: chemokine (C-C motif) receptor 7 [Par
 Length = 372

Score = 669 bits (1727), Expect = 0.0
 Identities = 342/372 (91%), Positives = 343/372 (92%)

Query: 7 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKA WFLPIMYS 66
 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKA WFLPIMYS
 Sbjct: 1 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKA WFLPIMYS 60

Query: 67 IICFXXXXXXXXXXTYIYFKRLKTM TDYLLNLA VADILFL LTPFWAYSAAKSWVFGV 126
 IICF TYIYFKRLKTM TDYLLNLA VADILFL LTPFWAYSAAKSWVFGV
 Sbjct: 61 IICFVGGLGNGLVVLTYIYFKRLKTM TDYLLNLA VADILFL LTPFWAYSAAKSWVFGV 120

Query: 127 HFCKLIFAIYKMSFFSGM LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILA 186
 HFCKLIFAIYKMSFFSGM LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVG ILA
 Sbjct: 121 HFCKLIFAIYKMSFFSGM LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILA 180

Query: 187 TVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMSFCYLVI 246
 TVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMSFCYLVI
 Sbjct: 181 TVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMSFCYLVI 240

Query: 247 IRTLLQARNFERNXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSSTCELSKQLNI 306
 IRTLLQARNFERN QLPYNGVVLAAQTVANFNITSSTCELSKQLNI
 Sbjct: 241 IRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAAQTVANFNITSSTCELSKQLNI 300

Query: 307 AYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKD LGCLSQEQLRQWSSCRHIRSSM 366
 AYDVTYSLACVRCCVNPFLYAFIGVKFRND+FKLFKD LGCLSQEQLRQWSSCRHIRSSM
 Sbjct: 301 AYDVTYSLACVRCCVNPFLYAFIGVKFRNDLFKLFKD LGCLSQEQLRQWSSCRHIRSSM 360

Query: 367 SVEAETTTTFSP 378
 SVEAETTTTFSP
 Sbjct: 361 SVEAETTTTFSP 372

 >gi|56553516|gb|AAV97930.1| chemokine receptor 7 [Bos taurus]

Length = 379

Score = 635 bits (1638), Expect = 0.0
 Identities = 319/379 (84%), Positives = 338/379 (89%), Gaps = 1/379 (0%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKA 60
 MDLGKPMK+VLVALLVIFQVCLCQDEVT+YIGDNTTVDYTL+ES+C KKDVRFKA 60
 Sbjct: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLYESVCFKKDVRNFKA 60

Query: 61 LPIMYSIICFXXXXXXXXTYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKMTDTYLLNLADILFLLTLPFWAYSAAK
 Sbjct: 61 LPIMYSIICFVGLLGNGLVMLYIYFKRLKMTDTYLLNLALADILFLLTLPFWAYSAAK 120

Query: 121 SWVFGVHFKLIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SWVFGVH CKLIF IYK+SFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC+
 Sbjct: 121 SWVFGVHVKLIFGIYKISFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC 180

Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLAMS 240
 G +LA VLS PE++YS +Q+SSSEQA+RCSL+TEHVEA ITIQAQMVGFL+PL+AMS
 Sbjct: 181 GIWMLAIVLSTPEVMSGIQKSSSEQALRCSLVTEHVEALITIQAQMVGFLIPLMAMS 240

Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSST-CE 299
 FCYLVIIRTLQARNFERN QLPYNGVVLATVANFNITS T CE
 Sbjct: 241 FCYLVIIRTLQARNFERNKAIVVIIAVVVVFVAFQLPYNGVVLAAHTVANFNITSGTSC 300

Query: 300 LSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCR 359
 LSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQEQLRQWS CR
 Sbjct: 301 LSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSFCR 360

Query: 360 HIRRSSSMSVEAETTTTFSP 378
 H RRSSSMSVEAETTTTFSP
 Sbjct: 361 HTRRSSSMSVEAETTTTFSP 379

 >gi|48374059|ref|NP_001001532.1| G chemokine (C-C motif) receptor 7 [Sus scrofa]
 gi|40363611|dbj|BAD06309.1| G chemokine (C-C motif) receptor 7 [Sus scrofa]
 gi|28569985|dbj|BAC57929.1| G chemokine receptor 7 [Sus scrofa]
 gi|28557110|dbj|BAC57561.1| G chemokine receptor 7 [Sus scrofa]

Length = 380

Score = 634 bits (1635), Expect = e-180
 Identities = 323/380 (85%), Positives = 337/380 (88%), Gaps = 2/380 (0%)

Query: 1 MDLGKPMK-SVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKA 59
 MDLGKPMK S+LVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTL+ES+C KKDVRFKA 60
 Sbjct: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLYESVCFKKDVRTFKA 60

Query: 60 FLPIIMYSIICFXXXXXXXXTYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAA 119
 FLPI+MYSIICF TYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAA
 Sbjct: 61 FLPVMYSIICFVGLLGNGLVMLYIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAA 120

Query: 120 KSWVFGVHFKLIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC 179
 KSWVFGVH CKLIF IYK+SFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC
 Sbjct: 121 KSWVFGVHVKLIFGIYKISFFSGMLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC 180

Query: 180 VGSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLAM 239
 VG +LA VLS PELLYS Q+SSSEQA+RCSLITEHVEA ITIQAQMVGFL+PL+AM
 Sbjct: 181 VGIWMLAMVLSTPELLYSGTQKSSSEQALRCSLITEHVEALITIQAQMVGFLIPLVAM 240

Query: 240 SFCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSST-C 298
 SFCYLVIIRTLQARNFERN QLPYNGVVLAAQTVANFNITS T C
 Sbjct: 241 SFCYLVIIRTLQARNFERNKAIKVIIAVVVVFVAFQLPYNGVVLAAQTVANFNITSGTSC 300

Query: 299 ELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSC 358
 ELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LRQWSSC
 Sbjct: 301 ELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSSC 360

Query: 359 RHIRRSSMSVEAETTTFSP 378
 RH RRSSMS EAETTTFSP
 Sbjct: 361 RHTRRSSMSAEAETTTFSP 380

 >gi|57091575|ref|XP_548131.1|  PREDICTED: similar to chemokine receptor 7 [Canis lupus familiaris]
 Length = 399

Score = 625 bits (1613), Expect = e-178
 Identities = 316/379 (83%), Positives = 333/379 (87%), Gaps = 1/379 (0%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAWF 60
 M LGKPMKS+LVVALLVIFQVCLCQDEVTDDYIG+NTTVDYTL+ES+C KKDKDVRNFKAWF
 Sbjct: 21 MQLGKPMKSLLVALLVIFQVCLCQDEVTDDYIGENTTDYTLYESVCFKKDVRNFKAWF 80

Query: 61 LPIMYSIICFXXXXXXXXXXTYIYFKRLKTMTDTYLLNLA+ADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKTMTDTYLLNLA+ADILFLLTLPFWAYSAAK
 Sbjct: 81 LPIMYSIICFMGLLGNGLVVLTYIYFKRLKTMTDTYLLNLA+ADILFLLTLPFWAYSAAK 140

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SW FGVH CK+IF IYK+SFFSGMLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCV
 Sbjct: 141 SWTFGVHVCKIIFGIYKISFFSGMLLL CISIDRYVAIVQAVSAHRHRARVLFISKLSCV 200

Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVIGFLVPLLAMS 240
 G +LA VLS PELLYS LQ+SSSEQA+RCSL T VEA ITIQAQMV+GFL+PL AMS
 Sbjct: 201 GIWMLAMVLSIPELLYSGLQKSSEQALRCSLNTNQEALITIQAQMVVGFLIPLGAMS 260

Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAAQTVANFNIT-SSTCE 299
 FCYLVIIRTLQARNFERN QLPYNGV+LAQTVANFNIT S +CE
 Sbjct: 261 FCYLVIIRTLQARNFERNKAIKVIIAVVVVFVAFQLPYNGVILAQTVANFNITGSGSCE 320

Query: 300 LSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSC 359
 LSKQLNIAYD+TYSLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQEQLRQWSSC
 Sbjct: 321 LSKQLNIAYDITYSLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSSC 380

Query: 360 HIRRSSMSVEAETTTFSP 378
 H RRSSMSVEAETTTFSP
 Sbjct: 381 HTRRSSMSVEAETTTFSP 399

 >gi|26332358|dbj|BAC29909.1|  unnamed protein product [Mus musculus]
 Length = 378

Score = 603 bits (1555), Expect = e-171
 Identities = 300/378 (79%), Positives = 326/378 (86%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAWF 60
 MD GKP K+LVVALLVIFQVC CQDEVTDDYIG+NTTVDYTL+ES+C KKDKDVRNFKAWF

Sbjct: 1 MDPGKPRKNLVVALLVIFQVCFQCDEVTDDYIGENTTVDYTLYESVCFKKDVRNFKAWF 60
 Query: 61 LPIMYSIICFXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLTLPLFWAYSAAK 120
 LP+MYS+ICF TYIYFKRLKTMTDTYLLNLAVADILFLLPFWAYS AK
 Sbjct: 61 LPLMYSVICFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLILPLFWAYSEAK 120
 Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SW+FGV+ CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV
 Sbjct: 121 SWIFGVYLCKGIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240
 G +LA LSIPELLYS LQ++S E +RCSL++ VEA ITIQAQMVGFLVPLLAMS
 Sbjct: 181 GIWMLALFISIPELLYSGLQKNSGEDTLRCSLVSAQVEALITIQAQMVGFLVPMIAMS 240
 Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYL+IIRTLQARNFERN QLPYNGVVLAQTVANFNIT+S+CE
 Sbjct: 241 FCYLIIRTLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCET 300
 Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLA VRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LR WSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRHWSSCRH 360
 Query: 361 IRRSSMSVEAETTTTFSP 378
 +R +S+S+EAETTTTFSP
 Sbjct: 361 VRNASVSMEEAETTTTFSP 378

>gi|6671772|ref|NP_031745.1| G chemokine (C-C motif) receptor 7 [Mus musculus]
 gi|468341|gb|AAA74232.1| G G protein-coupled receptor [Mus musculus]
 gi|1083330|pir||A55735 G protein-coupled receptor EBI1 - mouse
 gi|1352336|sp|P47774|CKR7_MOUSE G c-c chemokine receptor type 7 precursor (C-C CK
 (CCR-7) (MIP-3 beta receptor) (EBV-induced G
 protein-coupled receptor 1) (EBI1)
 Length = 378

Score = 601 bits (1550), Expect = e-171
 Identities = 299/378 (79%), Positives = 325/378 (85%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLESLCSKKDVRNFKAWF 60
 MD GKP K+VLVALLVIFQVC CQDEVTDDYIG+NTTVDYTLESLCSKKDVRNFKAWF
 Sbjct: 1 MDPGKPRKNLVVALLVIFQVCFQCDEVTDDYIGENTTVDYTLYESVCFKKDVRNFKAWF 60
 Query: 61 LPIMYSIICFXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLTLPLFWAYSAAK 120
 LP+MYS+ICF TYIYFKRLKTMTDTYLLNLAVADILFLLPFWAYS AK
 Sbjct: 61 LPLMYSVICFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLILPLFWAYSEAK 120
 Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SW+FGV+ CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV
 Sbjct: 121 SWIFGVYLCKGIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVGFLVPLLAMS 240
 G +LA LSIPELLYS LQ++S E +RCSL++ VEA ITIQAQMVGFLVPLLAMS
 Sbjct: 181 GIWMLALFISIPELLYSGLQKNSGEDTLRCSLVSAQVEALITIQAQMVGFLVPMIAMS 240
 Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYL+IIRTLQARNFERN QLPYNGVVLAQTVANFNIT+S+CE
 Sbjct: 241 FCYLIIRTLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCET 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLA VRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LR WSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRHWSSCRH 360

Query: 361 IRRSSMSVEAETTTFSP 378
 +R +S+S+EAETTTFSP
 Sbjct: 361 VRNASVSMEAETTTFSP 378

[>gi|58477681|gb|AAH89762.1| G Chemokine (C-C motif) receptor 7 [Rattus norvegicus]
 gi|41054914|ref|NP_955783.1| G chemokine (C-C motif) receptor 7 [Rattus norvegicus]
 gi|38570235|gb|AAR24573.1| G chemokine receptor 7-like protein [Rattus norvegicus]
 Length = 378

Score = 601 bits (1549), Expect = e-170
 Identities = 297/378 (78%), Positives = 325/378 (85%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCKKDVRNFKA 60
 MDLGKP K+VLVALLVIFQVC CQDEVTDDYIG+NTTVDYTL+ES+C KKDVRFKA 60
 Sbjct: 1 MDLGKPTKVNVLVALLVIFQVCFQCQDEVTDDYIGENTTVDYTLYESVCFKKDVRNFKA 60

Query: 61 LPIMYSIICFXXXXXXXXTYIYFKRLKTMTDYLLNLAVADILFLTLPLFWAYSAAK 120
 LP+MYS+ICF TYIYFKRLKTMTDYLLNLAVADILFL+ LPFWAYS AK
 Sbjct: 61 LPLMYSVICFVGLLGNGLVLTYYIYFKRLKTMTDYLLNLAVADILFLMILPLFWAYSEAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCV 180
 SW+FG + CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSC+
 Sbjct: 121 SWIFGAYLCKSIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCI 180

Query: 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQAQMVIGFLVPLLAMS 240
 G LA LSIPELLYS LQ++S E RCSL++ VEA I IQVAQM+GF++P+LAMS
 Sbjct: 181 GIWTLAFFLSIPELLYSGLQKNSGEDTWRCSDLVSAQVEALIAIQVAQMVGFLPMLAMS 240

Query: 241 FCYLVIIIRTLLQARNFERNXXXXXXXXXXXXQLPYNGVVLQAQTVANFNITSSTCEL 300
 FCYLVIIIRTLLQARNFERN QLPYNGVVLQAQTVANFNIT+S+CE
 Sbjct: 241 FCYLVIIIRTLLQARNFERNKAIVIIAVVVVFVVFQLPYNGVVLQAQTVANFNITNSSCEA 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLA VRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LRQWSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTFSP 378
 +R +S+S+EAETTTFSP
 Sbjct: 361 VRHTSVSMEAETTTFSP 378

[>gi|50760889|ref|XP_425875.1| G PREDICTED: similar to CC chemokine receptor 7 [C
 Length = 375

Score = 421 bits (1082), Expect = e-116
 Identities = 223/370 (60%), Positives = 272/370 (73%), Gaps = 8/370 (2%)

Query: 10 VLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCKKDVRNFKAFLPIMYSIIC 69
 VL++ L+ F + VTDDY NTT+DY +FE +C KK+VR+F+A FLP MYS+IC
 Sbjct: 13 VLLLCRLISF---CAGNNVTDDYDA-NTTIDYNMFEMMCEKKEVRDFRAAFLPAMYSILIC 68

Query: 70 FXXXXXXXXXXTYIYFKRLKTMTDYLLNLAVADILFLTLPLFWAYSAAKSWVFGVHFC 129

F TYIYFKRLKTM TD YLLNLA+ADILFLLTLPFWA SAA W FG C
 Sbjct: 69 FTGLLGNGLVMLTYIYFKRLKTM TD YLLNLA DILFLLTLPFWATSAATFWCFGEFAC 128

Query: 130 KLIFAIYKMSFFSGM LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVL 189
 K ++ I KMSFFSGM LLL CISIDRY AIVQA SAHR R R++ ISK++C+ +LA VL
 Sbjct: 129 KAVYCICKMSFFSGM LLLSISIDRYFAIVQAASAHRFRPRMIFISKVTCILIWLAFVL 188

Query: 190 SIPELLYSDLQRSSSEQAMRC SLITEHVEAFIT-IQVAQM VIGFLVPLLAMSFCYLVII R 248
 SIPEL++S + S RCS+I ++ F T I+V+QM V GFLVPL+ MS CYL+II+
 Sbjct: 189 SIPELVHSGVN NYDSHP--RCSIIASDLQT FSTGIKVSQMVFGFLVPLVVMSVCYLI IIK 246

Query: 249 TLLQARNFERNXXXXXXXXXXXXXX QLPYNGVVL AQT VANFNITSSTCELSKQLNIAY 308
 TLLQARNF E+ N QLPYNGV+LA+T++ FN TSS C+ SK+L++A
 Sbjct: 247 TLLQARNF EKNKAIKVIIAVVIVFVVFQLPYNGVMLAKTISVFNNNTSS-CDESKKLDMA D 305

Query: 309 DVTYSLACVRCCVN PFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRSSMSV 368
 DVTY+LAC RCC+NPFLYAFIGVKFRND+FKL K+LGCLSQ++L Q SSCR +R S ++
 Sbjct: 306 DVTYTLACFRCCLN PFLYAFIGVKFRNDLFKLLKE LGCLSQQLWQLSSCRESKRF SFAM 365

Query: 369 EAETTTTFSP 378
 E ETTTTFSP
 Sbjct: 366 ETETTTTFSP 375

 >gi|33415854|gb|AAQ18436.1|  G chemokine receptor 7 [Bos taurus]
 Length = 246

Score = 409 bits (1050), Expect = e-113
 Identities = 210/247 (85%), Positives = 222/247 (89%), Gaps = 2/247 (0%)

Query: 133 FAIYKMSFFSGM LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIP 192
 FAIYKMSFFSGM LLL CISIDRYVAIVQAVSAHRHRARVLLISKLSC+G +LA VLS P
 Sbjct: 1 FAIYKMSFFSGM LLL-CISIDRYVAIVQAVSAHRHRARVLLISKLSCLG IWLAI VLSTP 59

Query: 193 ELLYSDLQRSSSEQAMRC SLITEHVEAFITI QVAQM VIGFLVPLLAMSFCYLVII R TLLQ 252
 E++YS +Q+SSSEQA+RCSL+TEHVEA ITI QVAQM V+GFL+PL+AMSFCYLVII R TLLQ
 Sbjct: 60 EVMYSGI QKSSSEQALRCSL VTEHVEALITI QVAQM VVGFLIPLMAMSFCYLVII R TLLQ 119

Query: 253 ARNFERNXXXXXXXXXXXXXX QLPYNGVVL AQT VANFNITSST-CELSKQLNIAYDVT 311
 ARNFERN QLPYNGVVL AQT VANFNITS T CELSKQLNIAYDVT
 Sbjct: 120 ARNFERNKAIVVIIAVVVVFVAFQLPYNGVVL AQT VANFNITS GTSCELSKQLNIAYDVT 179

Query: 312 YSLACVRCCVN PFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAE 371
 YSLACVRCCVN PFLYAFIGVKFRND+FKL FKL DLGCLSQEQLRQWSSCRHIRSSMSVEAE
 Sbjct: 180 YSLACVRCCVN PFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAE 239

Query: 372 TTTTFSP 378
 TTTTFSP
 Sbjct: 240 TTTTFSP 246

 >gi|49118818|gb|AAH73273.1|  G MGC80638 protein [Xenopus laevis]
 Length = 358

Score = 375 bits (963), Expect = e-102
 Identities = 186/364 (51%), Positives = 251/364 (68%), Gaps = 7/364 (1%)

Query: 16 LVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAFLPIMYSIICFXXXXX 75
+ FQ+ + +D V+ D +T+DY+ +++C K DVR F++ FLP MY+IIC
Sbjct: 1 MATFQLAVGEDNVSTDENVPYSTMDYSDLQTCQKGDVRTFRSSFLPAMYTIICLVGLAG 60

Query: 76 XXXXXXXTYIYFKRLKTMTDYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAI 135
Y+YF RLK TD Y+LNLA+ADI+FLLTLPFWA S AK+WVFG CK+I+ +
Sbjct: 61 NGLVMIRYLYFNRLKNGTDYYMLNLAIADIVFLLTLPFWAVSVAKNWFVGSEMCKIIYCL 120

Query: 136 YKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELL 195
YKMSFFSGM LL+C+S++RY AIVQA SAHRHR++ +LISKLS +G + A +LSIPELL
Sbjct: 121 YKMSFFSGMFLLMCVSMERYFAIVQAPSAHRHRSKTVLISKLSSLGIVWFAGLSSIPELL 180

Query: 196 YSDLQRSSSEQAMRCSLITEHVEAF-ITIQVAQMVGFLVPLLAMSF CYLVIIRTLLQAR 254
YS + + C + + +++ +++++QM GF +PL+ M+ CY +IIR LLQAR
Sbjct: 181 YSGVNNNGG--VNMCIIFSNSIQSLSAKLKISQMFFGFFLPLIIMALCYCMIIRKLLQAR 238

Query: 255 NFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSL 314
NFE+ QLPYN V+L +T N + CE SK+L+IA DVTYSL
Sbjct: 239 NFEKYKAIKVIIIAIVIVFVAFQLPYNSVMLIKTFDN----GTDCEASKLDIADDVTYSL 294

Query: 315 ACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAETTT 374
AC RCC+NPFLYA IG+KFRND+ KLFKD+GCLSQE++ +WSS + RR+S +++ ETTT
Sbjct: 295 ACFRCCLNPDFLYAIIGIKFRNDLCKLFKDIGCLSQEKITEWSSAKPSRRTSFAMDTETTT 354

Query: 375 TFSP 378
TFSP
Sbjct: 355 TFSP 358

gi|47223975|emb|CAG06152.1| unnamed protein product [Tetraodon nigroviridis]
Length = 848

Score = 286 bits (731), Expect = 9e-76
Identities = 149/339 (43%), Positives = 205/339 (60%), Gaps = 9/339 (2%)

Query: 38 TVDYTLFESLCSKKDVRNFKAFLPIMYSIICFXXXXXXXXTYIYFKRLKTMTDTYL 97
T DY+ F ++C K+ R F+ WF+P YS+I F T+ YFKRLKTMTD YL
Sbjct: 1 TADYSTFPTVCVKELNRQFRRWFMPFTYSVIFFLGLAGNLLVILTFYYFKRLKTMTDVYL 60

Query: 98 LNLAVALDILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLCISIDRYVA 157
LNL+ AD+LF L+LPFWA + WV G C ++ +YK+SF+S M LL CIS+DRY A
Sbjct: 61 LNLSFADLLFALS LPFWAANTMTKWLGEEMCIAMYTVYKVSFYSSMFLCCISVDRYFA 120

Query: 158 IVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHV 217
I +A SA+R+R++ + +SK+S + A + S+PE+ Y+ + ++ C+ T
Sbjct: 121 ISKATSAYRYRSQTMFLSKVSSAVVVAALIFSMPEMRYTSVNNNT-----CTPYTGSK 174

Query: 218 EAF-ITIQVAQMVGFLVPLLAMSFCYLVIIRTLQARNFERNXXXXXXXXXXXXQ 276
+ + IQV Q+V+ F +PL+ MS CY II+TL QA+NFERN Q
Sbjct: 175 DQLRVIIQVGQIVLAFALPLVIMSICYSSIITLCQAQNFERNKAIVLAVVAVFLVSQ 234

Query: 277 LPYNGVVLAQTVANFNITSSTCELSKQLNIAVDVTYSIACVRCCVNPFLYAFIGVKFRND 336
+PYN V+ T+ +++C L A DVT LA RCC+NP +YAFIGVKFRND
Sbjct: 235 VPYNLVLFWSTLVTAKGGTTSCSYDNNLLYATDVTQCLAFFRCCLNPIVYAFIGVKFRND 294

Query: 337 IFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAETTTT 375
+ KL KD GC+S E +--+S R RRSS E ETTTT
Sbjct: 295 LLKLLKDWGCMSHESFFKYTSRR--RRSSGFTETETTTT 331

[>gi|14043042|ref|NP_112477.1| G chemokine (C-C motif) receptor 9 isoform A [Homo
 gi|46854634|gb|AAH69678.1| G Chemokine (C-C motif) receptor 9, isoform A [Homo sa
 gi|7673009|gb|AAF66699.1| G CC chemokine receptor 9A [Homo sapiens]
 gi|4886432|emb|CAB43477.1| G chemokine receptor CCR9 [Homo sapiens]
 Length = 369

Score = 251 bits (641), Expect = 2e-65
 Identities = 128/335 (38%), Positives = 198/335 (59%), Gaps = 16/335 (4%)

Query: 28 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAFLPIMYSIICFXXXXXXXXXT 82
 + DDY ++T+ V++ + C K +VR F + FLP +Y ++

Sbjct: 13 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 72

Query: 83 YIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFKLIFAIYKMSFFS 142
 Y Y R+KMTD +LLNLAD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S

Sbjct: 73 YWYCTRVKTMTDMFLNLAIADLLFLVTLFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 132

Query: 143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRS 202
 +LL++CIS+DRY+AI QA+ AH R + LL SK+ C +LA L IPE+LYS ++

Sbjct: 133 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAALCipeILYSQIKEE 192

Query: 203 SSEQAMRCISLI-----TEHVEAFITIQVAQMVGFLVPLLAMSFCYLVIIRTLLQARNF 256
 S C+++ T+ A +T++V ++GF +P + M+ CY +II TL+QA+

Sbjct: 193 SG--IAICTMVYPDESTKLKSAVLT--ILGFFLPFVVMACCYIIIHTLIQAKKS 247

Query: 257 ERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLAC 316
 ++ Q PYN ++L QT+ + + S C +S ++I + VT ++A

Sbjct: 248 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 307

Query: 317 VRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q

Sbjct: 308 FHSLNPVLYVFVGERFRRDLVKTLKNLGCISQAQ 342

[>gi|14043044|ref|NP_006632.2| G chemokine (C-C motif) receptor 9 isoform B [Homo
 gi|29825379|gb|AAO92294.1| G chemokine (C-C motif) receptor 9 [Homo sapiens]
 gi|7673011|gb|AAF66700.1| G CC chemokine receptor 9B [Homo sapiens]
 gi|1245055|gb|AAA93319.1| G GPR-9-6
 gi|1730237|sp|P51686|CKR9_HUMAN G C-C chemokine receptor type 9 (C-C CKR-9) (CC-C
 (GPR-9-6)
 Length = 357

Score = 251 bits (641), Expect = 2e-65
 Identities = 128/335 (38%), Positives = 198/335 (59%), Gaps = 16/335 (4%)

Query: 28 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAFLPIMYSIICFXXXXXXXXXT 82
 + DDY ++T+ V++ + C K +VR F + FLP +Y ++

Sbjct: 1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60

Query: 83 YIYFKRLKMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFKLIFAIYKMSFFS 142
 Y Y R+KMTD +LLNLAD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S

Sbjct: 61 YWYCTRVKTMTDMFLNLAIADLLFLVTLFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120

Query: 143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRS 202

+LL++CIS+DRY+AI QA+ AH R + LL SK+ C +LA L IPE+LYS ++
 Sbjct: 121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWLAAALCIPEILYSQIKEE 180

Query: 203 SSEQAMRCISL-----TEHVEAFITIQAQMVGFLVPLLAMSFCYLVIIRTLQARNF 256
 S C++ T+ A +T++V ++GF +P + M+ CY +II TL+QA+
 Sbjct: 181 SG--IAICTMVYPDESTKLKSAVTLKV--ILGFFLPFVVMACCYIIIHTLIQAKKS 235

Query: 257 ERNXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLAC 316
 ++ Q PYN ++L QT+ + + S C +S ++I + VT ++A
 Sbjct: 236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295

Query: 317 VRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQAO 330

 >gi|57101682|ref|XP_541909.1|  PREDICTED: similar to chemokine (C-C motif) receptor 9
 [Canis familiaris]
 Length = 642

Score = 250 bits (639), Expect = 4e-65
 Identities = 137/372 (36%), Positives = 208/372 (55%), Gaps = 15/372 (4%)

Query: 8 KSVLVVALLVIFQVCLCQDEVTDDYIGDNTTV--DYTLFESL-CSKKDVRNFKAWFPLIM 64
 K + +++V + ++DDY +T+ DY F L C K VR F + FLP +
 Sbjct: 268 KQACIWSIMVPTEFTNLISNISDDYSYHSTSPVDDYMNFPDLFCQKGHVRQFASHFLPPL 327

Query: 65 YSIICFXXXXXXXXTYIYFKRLKTMTDYLLNLAVADILFLTLPFWAYSAAKSWVF 124
 Y ++ Y Y R+KTMTD +LLNLA+AD+LFL TLPFWA +AA W F
 Sbjct: 328 YWLVFIVGTLGNSLVLVYCYCTRVKTMDFLLNLAIADLLFLTLPFWAIAAADQWKF 387

Query: 125 GVHFCKLIFAIYKMSFFSGMLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAI 184
 CK++ ++YKM+F+S +LL++CIS+DRY+AI QA A R + L+ SK+ C +
 Sbjct: 388 QTPLCKVNVNSMYKMNFYCVLLIMCISVDRYIAIAQATKAQWTWRQKRLVYSKMVCFTVWV 447

Query: 185 LATVLSIPELLYSDLQRSSSEQAMRCISL---TEHVEAFITIQAQMVGFLVPLLAMSF 241
 +A L IPELLYS L+ S C++ ++ + + +++++GF +P + M+
 Sbjct: 448 VAATLCIPELLYSQLKEES--DITICTMVYPSDQNSKVKSVVLTKVILGFFLPFVVMAC 505

Query: 242 CYLVIIRTLQARNFERNXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELS 301
 CY +II TLLQAR ++ Q PYN ++L QT+ + + S C +S
 Sbjct: 506 CYTIIYTLQARKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYTVFLSNCAIS 565

Query: 302 KQLNIAYDVTYSLACVRCCVNPFYAFIGVKFRNDIFKLFKDLGCLSSEQQLRQWSSCRH- 360
 ++I + VT ++A C+NP LY F+G +FR D+ K K LGC+SQE QW S
 Sbjct: 566 TNVDICFQVTQTIAFFHSCLNPVLYVFVGERFRRDLVKTLKSLGCISQE---QWVSFTRR 622

Query: 361 ---IRRSSMSVE 369
 ++ SSM +E
 Sbjct: 623 EGSVKLSSMILLE 634

 >gi|6753462|ref|NP_034043.1|  chemokine (C-C motif) receptor 9 [Mus musculus]
 gi|4886533|emb|CAB43480.1|  chemokine receptor CCR9 [Mus musculus]
 gi|7159932|emb|CAB66136.2|  CCR9 chemokine receptor [Mus musculus]
 gi|26341364|dbj|BAC34344.1|  unnamed protein product [Mus musculus]

gi|12859710|dbj|BAB31747.1| **G** unnamed protein product [Mus musculus]
 gi|8134364|sp|Q9WUT7|CKR9_MOUSE **G** C-C chemokine receptor type 9 (C-C CKR-9) (CC-C
 (Chemokine C-C receptor 10)
 Length = 369

Score = 247 bits (631), Expect = 3e-64
 Identities = 124/326 (38%), Positives = 192/326 (58%), Gaps = 11/326 (3%)

Query: 29 TDDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXTYIYFKR 88
 TDDY+ N + + C K +VR F + FLP +Y ++ Y Y R
 Sbjct: 25 TDDYMNLNFSFFF-----CKKNNVRQFASHFLPPLYWLVFIVGTLGNSLVILVYWYCTR 78

Query: 89 LKTM TDYLLNLAVADILFLLTPFWAYSAAKS WVFGVHFCKLIFAIYKMSFFSGM LLLL 148
 +KTM TD +LLNL A+AD+LFL TLPFWA +AA W+F CK++ ++YKM+F+S +LL++
 Sbjct: 79 VKTM TD MFLLNLAIA DLLFLATLPFWAIAAAAGQWMFQT FMCKVVNSMYK MNFYSCV LIM 138

Query: 149 CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSSEQAM 208
 CIS+DRY+AIVQA+ A R + LL SK+ C+ ++A VL PE+LYS Q S
 Sbjct: 139 CISVDRYIAIVQAMKAQVWRQKRLLYSKMVCITI WMAAVLCTPEILYS--QVSGESGIA 196

Query: 209 RCSLI---TEHVEAFITI QVAQM VIGFLVPLLAMSFCYLVII RTLLQARNFERNXXXXX 265
 C+++ ++ + + + ++ +GF +P + M+FCY +II TL+QA+ ++
 Sbjct: 197 TCTMVYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCY TIIIHTLVQAKKSSKH KALKVT 256

Query: 266 XXXXXXXXXXXX QLPYNGVVL AQT VANFNITSSTCELSKQLNIA YDVTYSLACVRCCVNPFL 325
 Q PYN +++ Q V + + S C +S ++I + VT ++A C+NP L
 Sbjct: 257 ITVLT VFIMS QFPYNSILVVQAVDAYAMFISNCTISTNIDICFQVTQ TIAFFHSCLN PVL 316

Query: 326 YAFIGVKFRNDIFKLFKDLGCLSSEQ 351
 Y F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 317 YVFVGERFRRDLVKTLK NLGCISQAO 342

gi|27229230|ref|NP_758832.1| **G** chemokine (C-C motif) receptor 9 [Rattus norvegicus]
 gi|25991905|gb|AAN76989.1| **G** chemokine receptor CCR9 [Rattus norvegicus]
 Length = 369

Score = 247 bits (630), Expect = 4e-64
 Identities = 127/330 (38%), Positives = 193/330 (58%), Gaps = 10/330 (3%)

Query: 30 DDYIGDNT--TV DY---TLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXYI 84
 DDY D+T T DY C K +VR F + FLP +Y ++ Y
 Sbjct: 15 DDYSYDSTASTDDYMNLNFSFFCKKNNVRQFASHFLPPLYWLVFVVGTVGN SLVILVY 74

Query: 85 YFKRLKTMTD TYLLNLAVADILFLLTPFWAYSAAKS WVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KTM TD +LLNL A+AD+LFL TLPFWA +AA W+F CK++ ++YKM+F+S +
 Sbjct: 75 YCTRVKTMTDMFLLNLAIADLFLATLPFWAIAAAAGQWMFQT FMCKVVNSMYK MNFYSCV 134

Query: 145 LLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSS 204
 LL++CIS+DRY+AIVQA+ A R + LL SK+ C+ ++A VL PE+LYS Q S
 Sbjct: 135 LLIMCISVDRYIAIVQAMKAQVWRQKRLLYSKMVCITI WMAAVLCTPEILYS--QISGE 192

Query: 205 EQAMRC SLI---TEHVEAFITI QVAQM VIGFLVPLLAMSFCYLVII RTLLQARNFERNXX 261
 C+++ ++ + + + ++ +GF +P + M+FCY +II TL+QA+ ++
 Sbjct: 193 SGIAICTMVYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCY TIIIHTLVQAKKSSKHKA 252

Query: 262 XXXXXXXXXXXX QLPYNGVVL AQT VANFNITSSTCELSKQLNIA YDVTYSLACVRCCV 321
 Q PYN +++ Q V + + S C +S ++I + VT ++A C+

Subjct: 253 LKVTITVLTVFIMSQFPYNCILVVQAVDAYTMFISNCTISTNIDICFQVTQTIAFFHSC 312

Query: 322 NPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351

NP LY F+G +FR D+ K K+LGC+SQ Q

Subjct: 313 NPVLYVFVGERFRRDLVKTLKNLGCISQAQ 342

[>gi|48675913|ref|NP_001001624.1| G chemokine C-C motif receptor 9 [Sus scrofa]
 gi|44890862|dbj|BAD12126.1| G chemokine C-C motif receptor 9 [Sus scrofa]
 gi|41688289|dbj|BAD08643.1| G chemokine (C-C motif) receptor 9 isoform A [Sus scrofa]
 Length = 369

Score = 245 bits (626), Expect = 1e-63

Identities = 130/333 (39%), Positives = 191/333 (57%), Gaps = 16/333 (4%)

Query: 30 DDYIGDNTTV----DYTLFESLCSKKDVRNFKAFLPIMYSIIICFXXXXXXXXTYI 84
 DDY D T +T + C K VR F + FLP +Y ++ Y

Subjct: 15 DDYGYDATPSIEDYGNFTFTDLFCKKNHVRQFASHFLPPLYWLVFIVGAVGNSLVILVYW 74

Query: 85 YFKRLKMTDTYLLNIAVADILFLLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S +

Subjct: 75 YCTRVKMTDMFLLNIAIDLLFLVTLFWAIAAAADQWKFQTFMCKVVNSMYKMNFYSCV 134

Query: 145 LLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSS 204
 LL++CIS+DRY+AI QA+ A R + LL SKL C ++A L IPELLYS Q

Subjct: 135 LLIMCISVDRYIAIAQAMRAQTWRQKRLYSKLVCFVWVMAAALCIPELLYS--QVKEE 192

Query: 205 EQAMRCISLI-----TEHVEAFITIQAQMVGFLVPLLAMSFCYLVIIRTLQARNFER 258
 C++ T A +T++V ++GF +P + M+ CY +II TL+QA+ +

Subjct: 193 HDIAICTMVYPSDESTNLKSAVLTQK---ILGFFLPVVMACCYTIIIHTLIQAKKSSK 249

Query: 259 NXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAVDVTYSLACVR 318
 + Q PYN V+L QT+ + + S+C +S ++I + VT ++A

Subjct: 250 HKALKVTITVLTVFVLSQFPYNCVLLQTVI DAYTMFISSCAVSTNIDICFQVTQTIAFFH 309

Query: 319 CCVNPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q

Subjct: 310 SCLNPVLYVFVGERFRRDLVKTLKNLGCISQAQ 342

[>gi|41688290|dbj|BAD08644.1| G chemokine (C-C motif) receptor 9 isoform B [Sus scrofa]
 Length = 357

Score = 245 bits (626), Expect = 1e-63

Identities = 130/333 (39%), Positives = 191/333 (57%), Gaps = 16/333 (4%)

Query: 30 DDYIGDNTTV----DYTLFESLCSKKDVRNFKAFLPIMYSIIICFXXXXXXXXTYI 84
 DDY D T +T + C K VR F + FLP +Y ++ Y

Subjct: 3 DDYGYDATPSIEDYGNFTFTDLFCKKNHVRQFASHFLPPLYWLVFIVGAVGNSLVILVYW 62

Query: 85 YFKRLKMTDTYLLNIAVADILFLLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S +

Subjct: 63 YCTRVKMTDMFLLNIAIDLLFLVTLFWAIAAAADQWKFQTFMCKVVNSMYKMNFYSCV 122

Query: 145 LLLL CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSS 204
 LL++CIS+DRY+AI QA+ A R + LL SKL C ++A L IPELLYS Q

Subjct: 123 LLIMCISVDRYIAIAQAMRAQTWRQKRLYSKLVCFVWVMAAALCIPELLYS--QVKEE 180

Query: 205 EQAMRCISLI-----TEHVEAFITIQAQMVGFLVPLLAMSF CYLVIIIRTLQARNFER 258
 C+++ T A +T++V ++GF P + M+ CY +II TL+QA+ +
 Sbjct: 181 HDIAICTMVPSDESTNLKSAVLTALKV---ILGFFLPFVVMACCYIIIHTLIQAKKSSK 237

Query: 259 NXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVR 318
 + Q PYN V+L QT+ + + S+C +S ++I + VT ++A
 Sbjct: 238 HKALKVTITVLTVFVLSQFPYNCVLLVQTIDAYTMFISSCAVSTNIDICFQVTQTIAFFH 297

Query: 319 CCVNPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 298 SCLNPVLYVFVGERFRRDLVKTLKNLGCISQAQ 330

>gi|34853814|ref|XP_217862.2| G similar to G protein-coupled receptor KY411 [Rat
 Length = 509

Score = 231 bits (590), Expect = 2e-59
 Identities = 131/355 (36%), Positives = 201/355 (56%), Gaps = 13/355 (3%)

Query: 35 DNTTVDYTLFESL--CSKKDVRNFKAWFLPIMYSIICFXXXXXXXXTYIYFKRLKTM 92
 D T DY++F CS ++VR+F F+PI YS+IC T+ ++K+ ++M
 Sbjct: 155 DYTGSDYSMFPETEPCSLQEVRDFTKVFVPIAYSLICVFGLLGNIMVVITFAFYKKARSM 214

Query: 93 TDTYLLNLAVADILFLLTPFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFGMLLLCIS 151
 TD YLLN+A+ DILF+LTLPFWA + A +W+FG CKL+ Y ++F GMLLL CIS
 Sbjct: 215 TDVYLLNMAITDILFVLTLPFWAVTHATDTWIFGNTMCKLMGTYAVNFNCGMLLACIS 274

Query: 152 IDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSSEQAM--R 209
 +DRY+AIVQA + R R+R L SK+ C+ ++ ++S P ++ + +
 Sbjct: 275 MDRYIAIVQATKSFRVRSRTLTHSKVICLTVWFVSIISPTFFFNKQYKLQGRDVCEPQ 334

Query: 210 CSLITEHVEAFITIQAQMVGFLVPLLAMSF CYLVIIIRTLQARNFERNXXXXXXXXX 269
 L++E + + +++ GF +PLL M FCYL II+TL+QA+N +R+
 Sbjct: 335 YKLVSEPIWKLLGMGLELLFGFFIPLLFMVF CYLFIKTLVQAQNSKRHRAIRVVIAVV 394

Query: 270 XXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFLYAFI 329
 Q+P+N +VL T AN +C K L A +V LA + CC+NP LYAFI
 Sbjct: 395 LVFLACQIPHNMVLLVTAANTGKMGRSCSAEKALAYARNVAEVLAFHCCLNPVLYAFI 453

Query: 330 GVKFRNDIFKLFKDLGCLSSEQ-----LRQWSSCRHIRRSSMSVEAETTTFS 377
 G KFR+ K+ KD+ C+ ++ R +S R++S +VE + ++F+
 Sbjct: 454 GQKFRSYFMKIMKDVWMRMRKSKVPTFFCARVYSESYISRQTSETVENDNASSFT 508

>gi|1668738|emb|CAB02144.1| G G PROTEIN-COUPLED RECEPTOR CKR-L3 [Homo sapiens]
 gi|2135142|pir||JCS068 G protein-coupled receptor CKR-L3 - human
 Length = 369

Score = 229 bits (584), Expect = 1e-58
 Identities = 130/352 (36%), Positives = 198/352 (56%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDNTTVDYTLFES--LCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXTYIYF 86
 ++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
 Sbjct: 10 SEDYFVSVNTSYYSDSEMLLCSLQEVROFSRLFVPIAYSLICVFGLLGNILVVITFAFY 69

Query: 87 KRLKTMTDTYLLNLAVADILFLLTPFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFGML 145

K+ ++MTD YLLN+A+ADILF+LTLPFWA S A +WVF CKL+ IY ++F GML
 Sbjct: 70 KKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGML 129

Query: 146 LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSSE 205
 LL CIS+DRY+AIVQA + R R+R L SK+ C+ L+ ++S +++ +
 Sbjct: 130 LLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLTVWGLSVIISSTFVNQKYNTQGS 189

Query: 206 QAM--RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLQARNFERNXXXX 263
 + ++E + + + +++ GF +PL+ M FCY I++TL+QA+N +R+
 Sbjct: 190 DVCEPKYQTVSEPIRKLLMLGLELLFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIR 249

Query: 264 XXXXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNP 323
 Q+P+N +VL T AN + +C+ K+ VT LA + CC+NP
 Sbjct: 250 VIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSQSEKLIGYTKTVTEVLAFLHCCINP 308

Query: 324 FLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAETTTT 375
 LYAFIG KFRN K+ KDL C+ ++ SC R S ++ +T+ T
 Sbjct: 309 VLYAFIGQKFRNYFLKILKDLWCVRKVKYKSSGFSC--AGRYSENISRQTSET 358

[>gi|37188165|ref|NP_113597.2| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|37187860|ref|NP_004358.2| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|29825375|gb|AAQ92293.1| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|23272703|gb|AAH37960.1| G Chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|9453791|emb|CAB99328.1| G GD:CCR6 [Homo sapiens]
 gi|2251211|gb|AAB62714.1| G GPR-CY4
 gi|2851567|sp|P51684|CKR6_HUMAN G C-C chemokine receptor type 6 (C-C CKR-6) (CC-C
 receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3)
 (CKR-L3) (DRY6)
 Length = 374

Score = 229 bits (584), Expect = 1e-58
 Identities = 130/352 (36%), Positives = 198/352 (56%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDNTTVDYTLFES--LCSKKDVRNFKAFLPIMYSIICFXXXXXXXXTYIYF 86
 ++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
 Sbjct: 15 SEDYFVSVNTSYYSVDSEMLLCSDLQEVRFQFSRLFVPIAYSPLICVFGLGNILVVITFAFY 74

Query: 87 KRLKTMDDTYLLNLAVALDILFLLTPFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGML 145
 K+ ++MTD YLLN+A+ADILF+LTLPFWA S A +WVF CKL+ IY ++F GML
 Sbjct: 75 KKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGML 134

Query: 146 LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSSE 205
 LL CIS+DRY+AIVQA + R R+R L SK+ C+ L+ ++S +++ +
 Sbjct: 135 LLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLTVWGLSVIISSTFVNQKYNTQGS 194

Query: 206 QAM--RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLQARNFERNXXXX 263
 + ++E + + + +++ GF +PL+ M FCY I++TL+QA+N +R+
 Sbjct: 195 DVCEPKYQTVSEPIRKLLMLGLELLFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIR 254

Query: 264 XXXXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNP 323
 Q+P+N +VL T AN + +C+ K+ VT LA + CC+NP
 Sbjct: 255 VIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSQSEKLIGYTKTVTEVLAFLHCCINP 313

Query: 324 FLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRSSMSVEAETTTT 375
 LYAFIG KFRN K+ KDL C+ ++ SC R S ++ +T+ T
 Sbjct: 314 VLYAFIGQKFRNYFLKILKDLWCVRKVKYKSSGFSC--AGRYSENISRQTSET 363

[gi|47221187|emb|CAG05508.1] unnamed protein product [Tetraodon nigroviridis]
Length = 277

Score = 229 bits (584), Expect = 1e-58
Identities = 117/252 (46%), Positives = 164/252 (65%), Gaps = 2/252 (0%)

Query: 88 RLKTM TDYLLNLA VADILFLLTPFWA YSAAKS WVF GVHF CKL IFAIY KMSFFSGMLL 147
RLKTM TDYLLNLA VAD+LFL TLPF A A K W FG+ CK + A+Y+++FFSGMLL
Sbjct: 23 RLKTM TDVYLLNLA VADLLFLCTLPFLA VEA IKYWNF GLAL CKTV LAVYR INF FSGMLL 82

Query: 148 LCISIDRYVAI VQAVSAH RHRARVLLIS KLSCV GSAILATV LSIPE LLYSDL QRS SSEQA 207
CIS+DRY++IVQ A + + L SKL C+ + + + T+L++PE +Y+ ++ +Q+
Sbjct: 83 TCISV DRYISIVQVTKA QNTKKQRLFW SKLICLIVW VV VSTLLALPE F IYARV KTK QRDQ S 142

Query: 208 MRCS LITEH VEA F I QV --AQ MVIGFLV P LAMSFC YL VI I RTLL QAR N FERN XXXXX 265
+ + ++ E I I V Q+ +GF +PL+ M FCY V+ I RTLL QAR N F++
Sbjct: 143 LCT LIYWDN S ENQ I K I L V L S I Q I C MGF WL P L M V M I F C Y S V V I R T L L QAR N F Q K H K A L R V I 202

Query: 266 XXXXXXXXXX QLPYNGV VLA QTVANF NITS STCE LS KQ L N I AY D V T Y S L A C V R C C V N P F L 325
QLPYN +++ +T N T S+CE L +A +T S L A C+NP F L
Sbjct: 203 FAVV L V F V L S QLPY N S L L I F E T T Q A A N T T M S S C E T R I N L E L A K Q I T K S L A Y A H A C L N P F L 262

Query: 326 YA FIG V K F R N D I 337
YA FIG V + F R D +
Sbjct: 263 YA FIG V R F R Q D L 274

[gi|55627742|ref|XP_527565.1] G PREDICTED: chemokine (C-C motif) receptor 6 [Par
Length = 522

Score = 228 bits (582), Expect = 2e-58
Identities = 130/352 (36%), Positives = 197/352 (55%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDNTTVDYTLFES--LCSKKDVRNFKA WFLPIM YSIICFXXXXXXXXTYIYF 86
++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
Sbjct: 163 SEDYF VSVNTSYY SVDSETLLCSLQEV RQFS RL FVPI AYSLIC VFG L GNIL VV ITFA FY 222

Query: 87 KRLKTMTD TYLLNLA VADILFLLTPFWA YSAAKS -WVFGVHF CKL IFAIY KMSFFGML 145
K+ ++MTD YLLN+A+ADILF+LTPFWA S A WVF CKL+ IY ++F GML
Sbjct: 223 KKAR SMTD VYLLNMAIADILF VLTLPFWA VSHATGVW VFSNATCKLLKG IYAINFNC GML 282

Query: 146 LL C I S I D RYVAI VQAVSAH RHRARVLLIS KLSCV GSAILATV LSIPE LLYSDL QRS SSEQA 205
LL CIS+DRY+AI VQ A + R R+R L SK+ C+ L+ ++S +++ +
Sbjct: 283 LLTC I SMD RYIAI VQATKS FRL R SRTL PR SKI I CLV W GLS V I S S S T F V FN Q KYNT QGS 342

Query: 206 QAM--RCS LITEH VEA F I T I Q V A Q M V I G F L V P L L A M S F C Y L V I I R T L L Q A R N F E R N X X X X 263
+ ++E + + + + + + GF +PL+ M FCY I++TL+QA+N +R+
Sbjct: 343 DVCEPKY QTVSEPI RWKLLMLG L E L L F G F F I P L M F M I F C Y T F I V K T L V Q A Q N S K R H K A I R 402

Query: 264 XXXXXXXXXX QLPYNGV VLA QTVANF NITS STCE LS KQ L N I AY D V T Y S L A C V R C C V N P 323
Q+P+N +VL T AN + +C+ K+ VT LA + CC+NP
Sbjct: 403 VIIAVV L V F L A C Q I P H N -M V L L V T A A N L G K M N R S C Q S E K L I G Y T K T V T E V I A F L H C C L N P 461

Query: 324 FLYA FIG V K F R N D I F K L F K D L G C L S Q E Q L R Q W S S C R H I R R S S M S V E A E T T T T 375
LYA FIG K F R N K+ K D L C+ ++ SC R S ++ +T+ T